

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: INFECTIO DIAGNOSTIC (I.D.I.) INC.
(B) STREET: 2050, BOULEVARD RENE LEVESQUE OUEST, 4E ETAGE
(C) CITY: STE-FOY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1V 2K8
(G) TELEPHONE: (418) 681-4343
(H) TELEFAX: (418) 681-5254

(A) NAME: BERGERON, MICHEL G.
(B) STREET: 2069 RUE BRULARD
(C) CITY: SILLERY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1T 1G2

(A) NAME: PICARD, FRANCOIS J.
(B) STREET: 1245, RUE DE LA SAPINIERE
(C) CITY: CAP-ROUGE
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1Y 1A1

(A) NAME: OUELLETTE, MARC
(B) STREET: 1035 DE PLOERMEL
(C) CITY: SILLERY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1S 3S1

(A) NAME: ROY, PAUL H.
(B) STREET: 28, RUE CHARLES GARNIER
(C) CITY: LORETTEVILLE
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G2A 3S1

(ii) TITLE OF INVENTION: SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL AND FUNGAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES ...

(iii) NUMBER OF SEQUENCES: 174

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(2) INFORMATION FOR SEO ID NO: 1:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

22

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

21

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

21

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Listeria monocytogenes*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATCCGATGAT GCTATGGCTT T

21

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Neisseria meningitidis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCAGCGGTAT TGTTTGGTGG T

21

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Neisseria meningitidis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CAGGCGGCCT TTAATAATTT C

21

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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"0021" E468660

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGATCGAATT CCACATGAAG GTTATTATGA

30

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGCTTCTCC CTCAACAATC AAATATCCT

30

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTCACCAGC TGTATTAGAA GTA

23

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*

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T002T1-1495650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTTCCCTGAA CATTATCTTT GAT

23

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CAAGAAGGTT GGTACAACC CAAAGA

26

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGGTCTTACC AGTAACTTTA CCGGAT

26

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TACTGACAAA CCATTCATGA TG

22

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

090964 1200
T002T 496660

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TRTGTGGTGT RATWGWCCA GGAGC

25

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACAACGTGGW CAAGTWTTAG CWGCT

25

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACCATTTTCWG TACCTTCTGG TAAGT

25

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAAATTGCAG GNAAATTGAT TGA

23

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(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTACGCATGG CNTGACTCAT CAT

23

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

03929643-12004
T0021T" 44962660

ACNKKKNACNG GNGTNGARAT GTT

23

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:18
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AYRTTNTTCNC CNGGCATNAC CAT

23

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCGCTTCTCC

10

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

| | |
|--|-----|
| TTCTTAGAGA CATTGAATAT GCCTTATGTC GGCGCAGGCG TATTGACCAG TGCATGTGCC | 60 |
| ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG GTGTGCCGCA AGTTCCTTAT | 120 |
| GTACCAGTAC TTAAGAATCA ATGGAAAAGAA AATCCTAAAA AAGTATTTGA TCAATGTGAA | 180 |
| GGTTCTTTGC TTTATCCGAT GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCCGCATT | 240 |
| ACAAAGGCAG AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT | 300 |
| TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC TGTATTAGGA | 360 |
| AATGAAGATG TTCGGACGAC TTTGCCTGGC GAAGTCGTAA AAGACGTAGC ATTCTATGAT | 420 |
| TATGAAGCCA AATATATCAA TAATAAAATC GAAATGCAGA TTCCAGCCGA AGTGCCGGAA | 480 |
| GAAGTTTATC AAAAAGCGCA AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC | 540 |
| GGATTGAGCC GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA | 600 |

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1920 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

| | |
|---|-----|
| GTGGGATTAA ACAGATTTAT GCGTGCGATG ATGGTGGTTT TCATTACTGC CAATTGCATT | 60 |
| ACGATTAACC CCGACATAAT ATTTGCAGCG ACAGATAGCG AAGATTCTAG TCTAAACACA | 120 |
| GATGAATGGG AAGAAGAAAA AACAGAAGAG CAACCAAGCG AGGTAAATAC GGGACCAAGA | 180 |
| TACGAAACTG CACGTGAAGT AAGTTCACGT GATATTAAAG AACTAGAAAA ATCGAATAAA | 240 |
| GTGAGAAATA CGAACAAAGC AGACCTAATA GCAATGTTGA AAGAAAAAGC AGAAAAAGGT | 300 |
| CCAAATATCA ATAATAACAA CAGTGAACAA ACTGAGAATG CGGCTATAAA TGAAGAGGCT | 360 |

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| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|------|
| TCAGGAGCCG | ACCGACCAGC | TATACAAGTG | GAGCGTCGTC | ATCCAGGATT | GCCATCGGAT | 420 |
| AGCGCAGCGG | AAATTAAAAA | AAGAAGGAAA | GCCATAGCAT | CATCGGATAG | TGAGCTTGAA | 480 |
| AGCCTTACTT | ATCCGGATAA | ACCAACAAAA | GTAAATAAGA | AAAAAGTGGC | GAAAGAGTCA | 540 |
| GTTGCGGATG | CTTCTGAAAG | TGACTTAGAT | TCTAGCATGC | AGTCAGCAGA | TGAGTCTTCA | 600 |
| CCACAACCTT | TAAAAGCAAA | CCAACAACCA | TTTTTCCCTA | AAGTATTTAA | AAAAATAAAA | 660 |
| GATGCGGGGA | AATGGGTACG | TGATAAAATC | GACGAAAATC | CTGAAGTAAA | GAAAGCGATT | 720 |
| GTTGATAAAA | GTGCAGGGTT | AATTGACCAA | TTATTAACCA | AAAAGAAAAG | TGAAGAGGTA | 780 |
| AATGCTTCGG | ACTTCCCGCC | ACCACCTACG | GATGAAGAGT | TAAGACTTGC | TTTGCCAGAG | 840 |
| ACACCAATGC | TTCTTGTTTT | TAATGCTCCT | GCTACATCAG | AACCGAGCTC | ATTCTGAATTT | 900 |
| CCACCACCAC | CTACGGATGA | AGAGTTAAGA | CTTGCTTTGC | CAGAGACGCC | AATGCTTCTT | 960 |
| GGTTTTAATG | CTCCTGCTAC | ATCGGAACCG | AGCTCGTTTC | AATTTCCACC | GCCTCCAACA | 1020 |
| GAAGATGAAC | TAGAAATCAT | CCGGGAAACA | GCATCCTCGC | TAGATTCTAG | TTTTACAAGA | 1080 |
| GGGGATTTAG | CTAGTTTGAG | AAATGCTATT | AATCGCCATA | GTCAAAATTT | CTCTGATTTT | 1140 |
| CCACCAATCC | CAACAGAAGA | AGAGTTGAAC | GGGAGAGGCG | GTAGACCAAC | ATCTGAAGAA | 1200 |
| TTTAGTTCGC | TGAATAGTGG | TGATTTTACA | GATGACGAAA | ACAGCGAGAC | AACAGAAGAA | 1260 |
| GAAATTGATC | GCCTAGCTGA | TTTAAGAGAT | AGAGGAACAG | GAAAACACTC | AAGAAATGCG | 1320 |
| GGTTTTTTTAC | CATTAAATCC | GTTTGCTAGC | AGCCCGGTTT | CTTCGTTAAG | TCCAAAGGTA | 1380 |
| TCGAAAATAA | GCGACCGGGC | TCTGATAAGT | GACATAACTA | AAAAAACGCC | ATTTAAGAAT | 1440 |
| CCATCACAGC | CATTAAATGT | GTTTAATAAA | AAAACACTAC | CGAAAACAGT | GAATAAAAAA | 1500 |
| CCAACCCCTG | TAAAGACCGC | ACCAAAGCTA | GCAGAACTTC | CTGCCACAAA | ACCACAAGAA | 1560 |
| ACCGTACTTA | GGGAAAATAA | AACACCCCTT | ATAGAAAAAC | AAGCAGAAAC | AAACAAGCAG | 1620 |
| TCAATTAATA | TGCCGAGCCT | ACCAGTAATC | CAAAAAGAAG | CTACAGAGAG | CGATAAAGAG | 1680 |
| GAAATGAAAC | CACAAACCGA | GGAAAAAATG | GTAGAGGAAA | GCGAATCAGC | TAATAACGCA | 1740 |
| AACGGAAAAA | ATCGTTCTGC | TGGCATTGAA | GAAGGAAAAA | TAATTGCTAA | AAGTGCAGAA | 1800 |
| GACGAAAAAG | CGAAGGAAGA | ACCAGGGAAC | CATACGACGT | TAATTCTTGC | AATGTTAGCT | 1860 |
| ATTGGCGTGT | TCTCTTTAGG | GGCGTTTATC | AAAATTATTC | AATTAAGAAA | AAATAATTAA | 1920 |

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

| | |
|---|-----|
| TACCGGTACG CTAAATATTG GTGATGTATT GGATATTATG ATTTGGGAAG CGCCGCCAGC | 60 |
| GGTATTGTTT GGTGGTGGCC TTTCTTCGAT GGGCTCGGGT AGTGCGCAAC AAACCAAGTT | 120 |
| GCCGGAGCAA CTGGTGACGG CACGTGGTAC GGTTCCTGTG CCGTTTGTTG GCGATATTTT | 180 |
| GGTGGTCGGT AAAACGCCTG GTCAGGTTCA GGAAATTATT AAAGGCCGCC TGAAAAAAT | 240 |
| GGCCAATCAG CCGCAAGTGA TGGTGCCTT GGTGCAGAAT AATGCGGCAA ATGTATCGGT | 300 |
| GATTCGCGCA GGCAATAGTG TCGTATGCC GTTGACGGCA GCCGGTGAGC GTGTGTTGGA | 360 |
| TGCGGTGGCT GCGGTAGGTG GTTCAACGGC AAATGTGCAG GATACGAATG TGCAG | 415 |

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

| | |
|---|-----|
| TCGCTTCTCC AGAAGAAATT TTAGAAACAT ATCTAGAAAA TCCCAAATTA GATAAACCGT | 60 |
| TTATATTATG TGAATACGCA CATGCAATGG GAAATTCACC AGGAGATCTT AATGCATATC | 120 |
| AAACATTAAT TGAAAAATAT GATAGTTTTA TTGGCGGTTT TGTTTGGGAA TGGTGTGATC | 180 |
| ATAGCATTCA GGTGAGGATA AAGGAAGGTA AACCAATTTT TAGATATGGT GGAGATTTTG | 240 |
| GTGAGGCCTT ACATGACGGT AATTTTTGTG TTGATGGTAT TGTTTCGCCA GATCGAATTC | 300 |
| CACATGAAGG TTATTATGAG TTAAACATG AACATAGACC TTTGAGATTG GTTAACGAAG | 360 |
| AGGATTATCG GTTTACATTG AAGAATCAAT TTGATTTTAC AAATGCGGAG GATAGTTTGA | 420 |
| TTGTTGAGGG AGAAGCGA | 438 |

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(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

| | |
|--|-----|
| ATGAACGTTA CACATATGAT GTATCTATCT GGAAGTCTAG TGGCTGGTGC ATTGTTATTT | 60 |
| TCACCAGCTG TATTAGAAGT ACATGCTGAT CAAGTGACAA CTCCACAAGT GGTAAATCAT | 120 |
| GTAAATAGTA ATAATCAAGC CCAGCAAATG GCTCAAAAGC TTGATCAAGA TAGCATTTCAG | 180 |
| TTGAGAAATA TCAAAGATAA TGTTCAGGGA ACAGATTATG AAAAACCAGT TAATGAGGCT | 240 |
| ATTACTAGCG TGGAAAAATT AAAGACTTCA TTGCGTGCCA ACCCTGAGAC AGTTTATGAT | 300 |
| TTGAATTCTA TTGGTAGTCG TGTAGAAGCC TTAACAGATG TGATTGAAGC AATCACTTTT | 360 |
| TCAACTCAAC ATTTAACAAA TAAGGTTAGT CAAGCAAATA TTGATATGGG ATTTGGGATA | 420 |
| ACTAAGCTAG TTATTCGCAT TTTAGATCCA TTTGCTTCAG TTGATTCAAT TAAAGCTCAA | 480 |
| GTTAACGATG TAAAGGCATT AGAACAAAAA GTTTTAACTT ATCCTGATTT AAAACCAACT | 540 |
| GATAGAGCTA CCATCTATAC AAAATCAAAA CTTGATAAGG AAATCTGGAA TACACGCTTT | 600 |
| ACTAGAGATA AAAAAGTACT TAACGTCAAA GAATTTAAAG TTTACAATAC TTAAATAAAA | 660 |
| GCAATCACAC ATGCTGTTGG AGTTCAGTTG AATCCAAATG TTACGGTACA ACAAGTTGAT | 720 |
| CAAGAGATTG TAACATTACA AGCAGCACTT CAAACAGCAT TAAAATAA | 768 |

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

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ATGAAAGTAG GTTTCGTCGG CTGGCGCGGT ATGGTCGGTT CGGTTTTGAT GCAGCGTATG 60
AAAGAAGAAA ACGACTTCGC CCACATTCCC GAAGCGTTTT TCTTTACCAC TTCCAACGTC 120
GGCGGCGCAC GCCCTGATTT CGGTCAGGCG GCTAAAACAT TATTGGACGC GAACAACGTT 180
GCCGAGCTGG CAAAAATGGA CATCATCGTT ACCTGCCAAG GCGGCGACTA CACCAAATCC 240
GTCTTCCAAG CCCTGCGCGA CAGCGGCTGG AACGGCTACT GGATTGACGC GGCATCCTCG 300
CTGCGTATGA AAGACGACGC GATTATCGTC CTCGACCCCG TCAACCGCAA CGTCATCGAC 360
AACGGCCTCA AAAACGGCGT GAAAACTAC ATCGGCGGCA ACTGTACCGT TTCCCTGATG 420
C 421

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTCATAGACG CTGAGCACGC TTTGGATCCA TCTTACGCGG CTGCTCTAGG TGTAATATT 60
GATGAGCTGT TGCTATCTCA ACCAGATTCT GGTGAGCAAG GTTTAGAAAT TGCAGGAAAA 120
TTGATTGACT CTGGGGCAGT TGATTTAGTT GTCATCGACT CTGTTGCAGC TCTTGATCCA 180
CGTGCGGAAA TCGATGGAGA TATCGGTGAT AGC 213

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GGGCCGGAAT CTTCTGGTAA GACAACTGTC GCTCTTCATG CTGCTGCTCA GGCGCAAAAA 60

0999943-112001
"TTTT" 4363660

| | |
|---|-----|
| GATGGCGGTA TTGCCGCTTT CATTGATGCA GAACATGCCC TTGATCCAGC CTATGCTGCT | 120 |
| GCTCTTGGCG TTAATATTGA TGAGCTTTTG CTTTCACAAC CAGATTCAGG AGAACAGGGT | 180 |
| CTTGAAATTG CAGGGAAATT GATTGATTCT GGCGCTGTTG ATTTAGTTGT TGTTGACTCA | 240 |
| GTGGCAGCTT TAGTACCACG TGCGGAGATT GACGGAGATA TTGGTAATAG TCATGTTGGC | 300 |
| TTACAAGCAC GCATGATGAG TCAAGCGATG CGTAAATTAT CAGCTTCAAT CAATAAAACA | 360 |
| AAAACCATTG CTATTTTTAT TAATCAATTG CGGGAAAAAG TTGGTATTAT GTTTGGTAAT | 420 |
| CCAGAAACAA CCCCTGGCGG GCGTGCCCTG AAGTTTTATT CTTCTGTGCG TCTTGATGTC | 480 |
| CGCGGCAATA CTCAAATTAA AGGAACCGGG GAACAAAAG ACAGCAATAT TGGTAAAGAG | 540 |
| ACCAAAATTA AAGTTGTTAA AAATAAGTT GCTCCACCAT TTAAGGAAGC TTTTGTAGAA | 600 |
| ATTATATATG GTGAAGGCAT TTCTCGTACA GGTGAATTAG TTAAGATTGC CAGTGATTTG | 660 |
| GGAATTATCC AAAAAGCTGG AGCTTGGTAC TC | 692 |

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

| | |
|---|-----|
| ATGGCGAAAA AACCAAAAAA ATTAGAAGAA ATTTCAAAAA AATTTGGGGC AGAACGTGAA | 60 |
| AAGGCCTTGA ATGACGCTCT TAAATTGATT GAGAAAGACT TTGGTAAAGG ATCAATCATG | 120 |
| CGTTTGGGTG AACGTGCGGA GCAAAAGGTG CAAGTGATGA GCTCAGGTTC TTTAGCTCTT | 180 |
| GACATTGCCC TTGGCTCAGG TGGTTATCCT AAGGGACGTA TCATCGAAAT CTATGGCCCA | 240 |
| GAGTCATCTG GTAAGACAAC GGTGCCCCTT CATGCAGTTG CACAAGCGCA AAAAGAAGGT | 300 |
| GGGATTGCTG CCTTTATCGA TGCGGAACAT GCCCTTGATC CAGCTTATGC TGCGGCCCTT | 360 |
| GGTGTCAATA TTGACGAATT GCTCTTGTCT CAACCAGACT CAGGAGAGCA AGGTCTTGAG | 420 |
| ATTGCGGGAA AATTGATTGA CTCAGGTGCA GTTGATCTTG TCGTAGTCGA CTCAGTTGCT | 480 |
| GCCCTTGTTT CTCGTGCGGA AATTGATGGA GATATCGGAG ATAGCCATGT TGGTTTGCAG | 540 |
| GCTCGTATGA TGAGCCAGGC CATGCGTAAA CTTGGCGCCT CTATCAATAA AACCAAAACA | 600 |

F00214 493666

ATTGCCATTT TTATCAACCA ATTGCGTGAA AAAGTTGGAG TGATGTTTGG AAATCCAGAA 660
 ACAACACCGG GCGGACGTGC TTTGAAATTC TATGCTTCAG TCCGCTTGGA TGTTCGTGGT 720
 AATACACAAA TTAAGGGAAC TGGTGATCAA AAAGAAACCA ATGTCGGTAA AGAAACTAAG 780
 ATTAAGGTTG TAAAAAATAA GGTAGCTCCA CCGTTTAAGG AAGCCGTAGT TGAAATTATG 840
 TACGGAGAAG GAATTTCTAA GACTGGTGAG CTTTGAAGA TTGCAAGCGA TTTGGATATT 900
 ATCAAAAAAG CAGGGGCTTG GTATTCTTAC AAAGATGAAA AAATTGGGCA AGGTTCTGAG 960
 AATGCTAAGA AATACTTGGC AGAGCACCCA GAAATCTTTG ATGAAATTGA TAAGCAAGTC 1020
 CGTTCTAAAT TTGGCTTGAT TGATGGAGAA GAAGTTTCAG AACCAAGATAC TGAAAAACAAA 1080
 AAAGATGAGC CAAAGAAAGA AGAAGCAGTG AATGAAGAAG TTCCGCTTGA CTTAGGCGAT 1140
 GAACTTGAAA TCGAAATTGA AGAATAAGCT GTTAAAGCAG TGGAGAAATC CGCTACTTTT 1200
 TCGA 1204

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGCGTTCAG GAAGTCTAGC TCTTGATATT GCTTGGATAG CTGGTGGTTA TCCTAAAGGA 60
 CGTATCATCG AAATCTATGG TCCAGAGTCT TCCGGTAAAA CGACTGTGGC TTTACATGCT 120
 GTAGCACAAG CTCAAAAAGA AGGTGGAATC GCAGCCTTTA TCGATGCCGA GCATGCGCTT 180
 GATCCAGCTT ATGCTGCTGC GCTTGGGGTT AATATTGATG AACTTCTCTT GTCTCAACCA 240
 GATTCTGGAG AACCAAGGACT TGAAATTGCA GGTAATTTGA TTGATTCTGG TGCGGTTGAC 300
 CTGGTTGTTG TCGATTCAAGT AGCAGCTTTA GTGCCACGTG CTGAAATTGA TGGTGATATT 360
 GGCGATAGCC ATGTCGGATT GCAAGCACGT ATGATGAGTC AGGCCATGCG TAAATTATCA 420
 GCTTCTATTA ATAAAACAAA AACTATCGCA ATCTTTATCA ACCAATTGCG TGAAAAAGTT 480
 GGTGTGATGT TTGGAAATCC TGAAACAACA CCAGGTGGTC GAGCTTTGAA ATTCTATGCT 540
 TCTGTTCCGC TGGATGTGCG TGGAAACAAC CAAATTAAAG GAACTGGTGA CAAAAGATA 600

09585643-112001

(2) INFORMATION FOR SEQ ID NO: 36:

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

(2) INFORMATION FOR SEQ ID NO: 37:

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

20

- (2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CGCAGTGTTA TCACTCATGG

20

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGAATGAAG CCATACCAAA

20

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ATCAGCAATA AACCAGCCAG

20

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TTACCATGAG CGATAACAGC

20

(2) INFORMATION FOR SEQ ID NO: 42:

09989643-12001
T002T "E4968660

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CTCATTTCAGT TCCGTTTCCC

20

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CAGCTGCTGC AGTGGATGGT

20

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CGCTCTGCTT TGTTATTCGG

20

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TACGCCAACA TCGTGGAAAG

20

(2) INFORMATION FOR SEQ ID NO: 46:

09989643-112001

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TTGAATTTGG CTTCTTCGGT

20

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGGATACAGA AACGGGACAT

20

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TAAATCTTTT TCAGGCAGCG

20

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GATGGTTTGA AGGGTTTATT ATAAG

25

(2) INFORMATION FOR SEQ ID NO: 50:

09989643-112001
"0021" 44968660

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

AATTTAGTGT GTTTAGAATG GTGAT

25

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ACTTCAACAC CTGCTGCTTT C

21

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TGACCACTTT TATCAGCAAC C

21

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGCAATAGTT GAAATGCTCG

20

(2) INFORMATION FOR SEQ ID NO: 54:

09039643-112001
100211 E4966660

(ii) MOLECULE TYPE: DNA (genomic)

CAGCTGTTAC AACGGACTGG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCTATGATCT CGCAGTCTCC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATCGTCACCG TAATCTGCTT

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CATTCTCGAT TGCTTTGCTA

20

(2) INFORMATION FOR SEQ ID NO: 58:

(ii) MOLECULE TYPE: DNA (genomic)

CCGAAATGCT TCTCAAGATA

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CTGGATTATG GCTACGGAGT

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGCAGTGTGA TGGTATCCAG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACTCTTGAT GAAGTGCTGG

20

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CTGGTCTATT CCTCGCACTC

20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

TATGAGAAGG CAGGATTCGT

20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCTTTCTCTC GAAGGCTTGT

20

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAGTTGCTGT TCAATGATCC

20

(2) INFORMATION FOR SEQ ID NO: 66:

0989643-12001
"TCTT" 002

(ii) MOLECULE TYPE: DNA (genomic)

GTGTTTGAAC CATGTACACG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGTAGAGGTC TAGCCCGTGT

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

ACGGGGATAA CGACTGTATG

20

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

ATAAAGATGA TAGGCCGGTG

20

(2) INFORMATION FOR SEQ ID NO: 70:

(ii) MOLECULE TYPE: DNA (genomic)

TGCTGTCATA TTGTCTTGCC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATTATCTTCG GCGGTTGCTC

20

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GACTATCGGC TTCCCATTC

20

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGATAGAAGC AGCAGGACAA

20

(2) INFORMATION FOR SEQ ID NO: 74:

(ii) MOLECULE TYPE: DNA (genomic)

CTGATGGATG CGGAAGATAC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GCCTTATGTA TGAACAAATG G

21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GTGACTTTWG TGATCCCTTT TGA

23

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TCCAATCATT GCACAAAATC

20

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AATTCCTCT ATTTGGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TCCCAAGCCA GTAAAGCTAA

20

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TGGTTTTTCA ACTTCTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

TCATAGAATG GATGGCTCAA

20

(2) INFORMATION FOR SEQ ID NO: 82:

0908943-11200
T00277-2455550

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

AGCTACTATT GCACCATCCC

20

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CAATAAGGGC ATACCAAAAA TC

22

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CCTTAACATT TGTGGCATT TC

22

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TTGGGAAGAT GAAGTTTTTA GA

22

(2) INFORMATION FOR SEQ ID NO: 86:

099394-12001
"E4968660"

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CCTTTACTCC AATAATTTGG CT

22

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TTTCATCTAT TCAGGATGGG

20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GGAGCAACAT TCTTTGTGAC

20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TGTGCCTGAA GAAGGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 90:

0909643-12001
FOOT" 2496860

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CGTGTTACTT CACCACCACT

20

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TATCTTATCG TTGAGAAGGG ATT

23

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CTACACTTGG CTTAGGATGA AA

22

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CTATCTGATT GTTGAAGAAG GATT

24

(2) INFORMATION FOR SEQ ID NO: 94:

090904 1300
T00211 24968660

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GTTTACTCTT GGTTTAGGAT GAAA

24

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CTTGTTGATC ACGATAATTT CC

22

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

ATCTTTTAGC AAACCCGTAT TC

22

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AACAGGTGAA TTATTAGCAC TTGTAAG

27

(2) INFORMATION FOR SEQ ID NO: 98:

090904.12001
100211 14968660

(ii) MOLECULE TYPE: DNA (genomic)

ATTGCTGTTA ATATTTTTTG AGTTGAA

27

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GTGATCGAAA TCCAGATCC

19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

ATCCTCGGTT TTCTGGAAG

19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTGGTCATAC ATGTGATGG

19

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

GATGTTACCC GAGAGCTTG

19

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTAAGCGTGC ATAATAAGCC

20

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TTGCGATTAC TTCGCCAACT

20

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TTTACTAAGC TTGCCCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 106:

09989643-12001
T00211-1496860

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AAAAGGCAGC AATTATGAGC

20

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:18
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:21
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

AAYATGATNA CNGGNGCNGC NCARATGGA

29

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

09585643-112001

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CCNACNGTNC KNCCRCCTC RCG

23

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

090213 112001

(D) OTHER INFORMATION:/note= "n = inosine"

CARYTNATHG TNGCNGTNAA YAARATGGA

29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

| | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|-----|
| ATGAAAAACA | CAATACATAT | CAACTTCGCT | ATTTTTTTAA | TAATTGCAAA | TATTATCTAC | 60 |
| AGCAGCGCCA | GTGCATCAAC | AGATATCTCT | ACTGTTGCAT | CTCCATTATT | TGAAGGAACT | 120 |
| GAAGGTTGTT | TTTTACTTTA | CGATGCATCC | ACAAACGCTG | AAATTGCTCA | ATTCAATAAA | 180 |
| GCAAAGTGTG | CAACGCAAAT | GGCACCAGAT | TCAACTTTCA | AGATCGCATT | ATCACTTATG | 240 |
| GCATTTGATG | CGGAAATAAT | AGATCAGAAA | ACCATATTCA | AATGGGATAA | AACCCCCAAA | 300 |
| GGAATGGAGA | TCTGGAACAG | CAATCATACA | CCAAAGACGT | GGATGCAATT | TTCTGTTGTT | 360 |
| TGGGTTTCGC | AAGAAATAAC | CCAAAAAATT | AGATTAAATA | AAATCAAGAA | TTATCTCAAA | 420 |
| GATTTTGATT | ATGGAAATCA | AGACTTCTCT | GGAGATAAAG | AAAGAAACAA | CGGATTAACA | 480 |
| GAAGCATGGC | TCGAAAGTAG | CTTAAAAAATT | TCACCAGAAG | AACAAATTCA | ATTCCCTGCGT | 540 |
| AAAATTATTA | ATCACAATCT | CCCAGTTAAA | AACTCAGCCA | TAGAAAACAC | CATAGAGAAC | 600 |
| ATGTATCTAC | AAGATCTGGA | TAATAGTACA | AAACTGTATG | GGAAAAC TGG | TGCAGGATTC | 660 |
| ACAGCAAATA | GAACCTTACA | AAACGGATGG | TTTGAAGGGT | TTATTATAAG | CAAATCAGGA | 720 |
| CATAAATATG | TTTTTGTGTC | CGCACTTACA | GGAAACTTGG | GGTCGAATTT | AACATCAAGC | 780 |
| ATAAAAGCCA | AGAAAAATGC | GATCACCATT | CTAAACACAC | TAAATTTATA | A | 831 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

| | |
|---|-----|
| TTGAAAAAGT TAATATTTTT AATTGTAATT GCTTTAGTTT TAAGTGCATG TAATTCAAAC | 60 |
| AGTTCACATG CCAAAGAGTT AAATGATTTA GAAAAAAAT ATAATGCTCA TATTGGTGTT | 120 |
| TATGCTTTAG ATACTAAAAG TGGTAAGGAA GTAAAATTTA ATTCAGATAA GAGATTTGCC | 180 |
| TATGCTTCAA CTTCAAAGC GATAAATAGT GCTATTTTGT TAGAACAAGT ACCTTATAAT | 240 |
| AAGTTAAATA AAAAAGTACA TATTAACAAA GATGATATAG TTGCTTATTC TCCTATTTTA | 300 |
| GAAAAATATG TAGGAAAAGA TATCACTTTA AAAGCACTTA TTGAGGCTTC AATGACATAT | 360 |
| AGTGATAATA CAGCAAACAA TAAAATTATA AAAGAAATCG GTGGAATCAA AAAAGTTAAA | 420 |
| CAACGTCTAA AAGAACTAGG AGATAAAGTA ACAAATCCAG TTAGATATGA GATAGAATTA | 480 |
| AATTACTATT CACCAAAGAG CAAAAAAGAT ACTTCAACAC CTGCTGCTTT CGGTAAGACT | 540 |
| TTAAATAAAC TTATCGCAA TGGAAAATTA AGCAAAGAAA ACAAAAAATT CTTACTTGAT | 600 |
| TTAATGTTAA ATAATAAAG CGGAGATACT TTAATTAAAG ACGGTGTTCC AAAAGACTAT | 660 |
| AAGGTTGCTG ATAAAAGTGG TCAAGCAATA ACATATGCTT CTAGAAATGA TGTGCTTTT | 720 |
| GTTTATCCTA AGGGCCAATC TGAACCTATT GTTTTAGTCA TTTTACGAA TAAAGACAAT | 780 |
| AAAAGTGATA AGCCAAATGA TAAGTTGATA AGTGAAACCG CCAAGAGTGT AATGAAGGAA | 840 |
| TTTTAA | 846 |

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

| | |
|---|-----|
| ATGTCCGCGA GCACCCCCC CATAACTCTT CGCCTCATGA CCGAGCGCGA CCTGCCGATG | 60 |
| CTCCATGACT GGCTCAACCG GCCGCACATC GTTGAGTGGT GGGGTGGCGA CGAAGAGCGA | 120 |
| CCGACTCTTG ATGAAGTGCT GGAACACTAC CTGCCCAGAG CGATGGCGGA AGAGTCCGTA | 180 |
| ACACCGTACA TCGCAATGCT GGGCGAGGAA CCGATCGGCT ATGCTCAGTC GTACGTCGCG | 240 |
| CTCGGAAGCG GTGATGGCTG GTGGGAAGAT GAAACTGATC CAGGAGTGCG AGGAATAGAC | 300 |
| CAGTCTCTGG CTGACCCGAC ACAGTTGAAC AAAGGCCTAG GAACAAGGCT TGTCCGCGCT | 360 |

T002111 112001

| | |
|--|-----|
| CTCGTTGAAC TACTGTTCTC GGACCCACACC GTGACGAAGA TTCAGACCGA CCCGACTCCG | 420 |
| AACAACCATC GAGCCATACG CTGCTATGAG AAGGCAGGAT TCGTGCGGGA GAAGATCATC | 480 |
| ACCACGCCTG ACGGGCCGGC GGTTTACATG GTTCAAACAC GACAAGCCTT CGAGAGAAAG | 540 |
| CGCGGTGTTG CCTAA | 555 |

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

| | |
|---|-----|
| ATGAACCAGA AAAACCCTAA AGACACGCAA AATTTTATTA CTTCTAAAAA GCATGTAAAA | 60 |
| GAAATATTGA ATCACACGAA TATCAGTAAA CAAGACAACG TAATAGAAAT CGGATCAGGA | 120 |
| AAAGGACATT TTACCAAAGA GCTAGTCAAA ATGAGTCGAT CAGTTACTGC TATAGAAATT | 180 |
| GATGGAGGCT TATGTCAAGT GACTAAAGAA GCGGTAAACC CCTCTGAGAA TATAAAAGTG | 240 |
| ATTCAAACGG ATATTCTAAA ATTTTCCTTC CCAAAACATA TAAACTATAA GATATATGGT | 300 |
| AATATTCCTT ATAACATCAG TACGGATATT GTCAAAAGAA TTACCTTTGA AAGTCAGGCT | 360 |
| AAATATAGCT ATCTTATCGT TGAGAAGGGA TTTGCGAAAA GATTGCAAAA TCTGCAACGA | 420 |
| GCTTTGGGTT TACTATTAAT GGTGGAGATG GATATAAAAA TGCTCAAAAA AGTACCACCA | 480 |
| CTATATTTTC ATCCTAAGCC AAGTGTAAGC TCTGTATTGA TTGTTCTTGA ACGACATCAA | 540 |
| CCATTGATTT CAAAGAAGGA CTACAAAAAG TATCGATCTT TTGTTTATAA GTGGGTAAAC | 600 |
| CGTGAATATC GTGTTCTTTT CACTAAAAAC CAATTCCGAC AGGCTTTGAA GCATGCAAAT | 660 |
| GTCATAATA TTAATAAACT ATCGAAGGAA CAATTTCTTT CTATTTTCAA TAGTTACAAA | 720 |
| TTGTTTCACT AA | 732 |

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

09959643-1-2001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

| | |
|--|-----|
| ATGAACAAAA ATATAAAATA TTCTCAAAAC TTTTAAACGA GTGAAAAAGT ACTCAACCAA | 60 |
| ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT ACGAAATTGG AACAGGTAAA | 120 |
| GGGCATTTAA CGACGAAACT GGCTAAAATA AGTAAACAGG TAACGTCTAT TGAATTAGAC | 180 |
| AGTCATCTAT TCAACTTATC GTCAGAAAAA TAAAAATCGA ATACTCGTGT CACTTTAATT | 240 |
| CACCAAGATA TTCTACAGTT TCAATTCCTT AACAAACAGA GGTATAAAAT TGTGGGAAT | 300 |
| ATTCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGGAAAG CCATGCGTCT | 360 |
| GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA CCTTGGATAT TCACCGAACA | 420 |
| CTAGGGTTGC TCTTGCACAC TCAAGTCTCG ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA | 480 |
| TGCTTTTCATC CTAAACCAAG AGTAAACAGT GTCTTAATAA AACTTACCCG CCATACCACA | 540 |
| GATGTTCCAG ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAAATG GGTCAATCGA | 600 |
| GAATATCGTC AACTGTTTAC TAAAAATCAG TTTCATCAAG CAATGAAACA CGCCAAAGTA | 660 |
| AACAATTTAA GTACCGTTAC TTATGAGCAA GTATTGTCTA TTTTAAATAG TTATCTATTA | 720 |
| TTTAACGGGA GGAAATAA | 735 |

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

| | |
|--|-----|
| ATGAACGAGA AAAATATAAA ACACAGTCAA AACTTTATTA CTTCAAAAACA TAATATAGAT | 60 |
| AAAATAATGA CAAATATAAG ATTAAATGAA CATGATAATA TCTTTGAAAT CGGCTCAGGA | 120 |
| AAAGGGCATT TTACCCTTGA ATTAGTACAG AGGTGTAATT TCGTAACTGC CATTGAAATA | 180 |
| GACCATAAAT TATGCAAAAC TACAGAAAAT AAACCTTGTTG ATCACGATAA TTTCCAAGTT | 240 |
| TTAAACAAGG ATATATTGCA GTTTAAATTT CCTAAAAACC AATCCTATAA AATATTTGGT | 300 |
| AATATACCTT ATAACATAAG TACGGATATA ATACGCAAAA TTGTTTTTGA TAGTATAGCT | 360 |
| GATGAGATTT ATTTAATCGT GGAATACGGG TTTGCTAAAA GATTATTAAA TACAAAACGC | 420 |
| TCATTGGCAT TATTTTAAAT GGCAGAAGTT GATATTTCTA TATTAAGTAT GGTTCGAAGA | 480 |

GAATATTTTC ATCCTAAACC TAGAGTGAAT AGCTCACTTA TCAGATTAAA TAGAAAAAAA 540
TCAAGAATAT CACACAAAGA TAAACAGAAG TATAATTATT TCGTTATGAA ATGGGTTAAC 600
AAAGAATACA AGAAAAATATT TACAAAAAAT CAATTTAACA ATTCCTTAAA ACATGCAGGA 660
ATTGACGATT TAAACAATAT TAGCTTTGAA CAATTCTTAT CTCTTTTCAA TAGCTATAAA 720
TTATTTAATA AGTAA 735

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

ATGAATAAAA TAAAAGTCGC AATTATCTTC GGCGGTTGCT CGGAGGAACA TGATGTGTCG 60
GTAAAATCCG CAATAGAAAT TGCTGCGAAC ATTAATACTG AAAAATTCGA TCCGCACTAC 120
ATCGGAATTA CAAAAACGG CGTATGGAAG CTATGCAAGA AGCCATGTAC GGAATGGGAA 180
GCCGATAGTC TCCCCGCCAT ATTCTCCCCG GATAGGAAAA CGCATGGTCT GCTTGTCATG 240
AAAGAAAGAG AATACGAAAC TCGGCGTATT GACGTGGCTT TCCCGGTTTT GCATGGCAAA 300
TGCGGGGAGG ATGGTGCGAT ACAGGGTCTG TTTGAATTGT CTGGTATCCC CTATGTAGGC 360
TGCGATATTC AAAGCTCCGC AGCTTGCAATG GACAAATCAC TGGCCTACAT TCTTACAAAA 420
AATGCGGGCA TCGCCGTCCC CGAATTTCAA ATGATTGAAA AAGGTGACAA ACCGGAGGCG 480
AGGACGCTTA CCTACCCTGT CTTTGTGAAG CCGGCACGGT CAGGTTTCGTC CTTTGGCGTA 540
ACCAAAGTAA ACAGTACGGA AGAACTAAAC GCTGCGATAG AAGCAGCAGG ACAATATGAT 600
GGAAAAATCT TAATTGAGCA AGCGATTTTCG GGCTGTGAGG TCGGCTGCGC GGTTCATGGGA 660
AACGAGGATG ATTTGATTGT CGGCGAAGTG GATCAAATCC GGTGAGCCA CGGTATCTTC 720
CGCATCCATC AGGAAAACGA GCCGGAAAAA GGCTCAGAGA ATGCGATGAT TATCGTTCCA 780
GCAGACATTC CGGTCGAGGA ACGAAATCGG GTGCAAGAAA CGGCAAAGAA AGTATATCGG 840
GTGCTTGGAT GCAGAGGGCT TGCTCGTGTT GATCTTTTTT TGCAGGAGGA TGGCGGCATC 900
GTTCTAAACG AGGTCAATAC CCTGCCCGGT TTTACATCGT ACAGCCGCTA TCCACGCATG 960
GCGGCTGCCG CAGGAATCAC GCTTCCCGCA CTAATTGACA GCCTGATTAC ATTGGCGATA 1020

099643-12001

GAGAGGTGA

1029

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATGAAAAAAAA TTGCCGTTTT ATTTGGAGGG AATTCTCCAG AATACTCAGT GTCACTAACC 60
TCAGCAGCAA GTGTGATCCA AGCTATTGAC CCGCTGAAAT ATGAAGTAAT GACCATTGGC 120
ATCGCACCAA CAATGGATTG GTATTGGTAT CAAGGAAACC TCGCGAATGT TCGCAATGAT 180
ACTTGGCTAG AAGATCACAA AACTGTCCAC CAGCTGACTT TTTCTAGCCA AGGATTTATA 240
TTAGGAGAAA AACGAATCGT CCCTGATGTC CTCTTTCCAG TCTTGCATGG GAAGTATGGC 300
GAGGATGGCT GTATCCAAGG ACTGCTTGAA CTAATGAACC TGCCTTATGT TGGTTGCCAT 360
GTCGCTGCCT CCGCATTATG TATGAACAAA TGGCTCTTGC ATCAACTTGC TGATACCATG 420
GGAATCGCTA GTGCTCCAC TTTGCTTTTA TCCCGCTATG AAAACGATCC TGCCACAATC 480
GATCGTTTTTA TTCAAGACCA TGGATTCCCG ATCTTTATCA AGCCGAATGA AGCCGGTTCT 540
TCAAAAGGGA TCACAAAAGT AACTGACAAA ACAGCGCTCC AATCTGCATT AACGACTGCT 600
TTTGCTTACG GTTCTACTGT GTTGATCCAA AAGGCGATAG CGGGTATTGA AATTGGCTGC 660
GGCATCTTAG GAAATGAGCA ATTGACGATT GGTGCTTGTC ATGCGATTTC TCTTGTCGAC 720
GGTTTTTTTTG ATTTTGAAGA GAAATACCAA TTAATCAGCG CCACGATCAC TGTCCCAGCA 780
CCATTGCCTC TCGCGCTTGA ATCAGATC AAGGAGCAGG CACAGCTGCT TTATCGAAAC 840
TTGGGATTGA CGGGTCTGGC TCGAATCGAT TTTTTCGTCA CCAATCAAGG AGCGATTTAT 900
TTAAACGAAA TCAACACCAT GCCGGGATTT ACTGGGCACT CCCGCTACCC AGCTATGATG 960
GCGGAAGTCG GGTATCCTA CGAAATATTA GTAGAGCAAT TGATTGCACT GGCAGAGGAG 1020
GACAAACGAT G 1031

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

0998941200
T002T "E496860

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia adiacens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

| | |
|---|-----|
| TGGTGCTATC TTAGTAGTAT CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACACAT | 60 |
| CTTATTATCA CGTCAAGTAG GTGTTCTTA CATCGTTGTA TTCTTAAACA AAGTTGACAT | 120 |
| GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA | 180 |
| ATACGATTTT CCAGGCGATG ACACTCCAGT TGTGTCAGGT TCTGCTTTAC GCGCTTTAGA | 240 |
| AGGCGACGCT TCATACRAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATACAT | 300 |
| TCCAACCTCA GAACGYGACG TTGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTTCTC | 360 |
| AATCACAGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA CGTGGACAAG TTCGTGTTGG | 420 |
| TGACGAAGTT GAAATCGTTG GTATTTTACA AGAACTTCA AAAACAACTG TAACTGGTGT | 480 |
| TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCAGGG GATAACATTG GTACATTATT | 540 |
| ACGTGGTGTT ACACGTGACA ACATCGAAGC TGGACAAGTT CTTGCTAAAC CAGGAACAAT | 600 |
| CACTCCACAT ACTAAATTCA AAGCTGAAGT TTACGTATTA ACTAAAGAAG AAGGTGGACG | 660 |
| TCATACTCCA TTCTTCTCTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACATCAC | 720 |
| TGGTGTTTGT GTGTTACCAG AAGGCGTTGA AATGGTAATG CCTGGTGATA ACGTAACTAT | 780 |
| GGAAGTTGAA TTAATTCACC CAGTAGCGA | 809 |

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia defectiva*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

| | |
|---|-----|
| CGGCGCGATC CTCGTTGTAT CTGCTGCTGA CGGCCCAATG CCACAAACTC GTGAACACAT | 60 |
| CCTCTTGTCT CGTCAAGTTG GTGTTCTTA CATCGTAGTA TTCTTGAACA AAGTTGACAT | 120 |

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GGTTGACGAC GAAGAATTGC TCGAATTAGT TGAAATGGAA GTTCGTGACC TCTTGTCTGA 180
 ATACGACTTC CCAGGCGACG ACACTCCAGT TATCGCTGGT TCAGCTTTGA AAGCTTTAGA 240
 AGGCGACGCT AACTACGAAG CTAAAGTTTT AGAATTGATG GAACAAGTTG ATGCTTACAT 300
 TCCAGAACCA GAACGTGACA CTGACAAGCC ATTCATGATG CCAGTCGAAG ACGTATTCTC 360
 TATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA CGTGGTCAAG TTCGCGTTGG 420
 TGACGAAGTT GAAATCGTTG GTATCGAAGA AGAACTTCT AAGACTACCG TTACCGGTGT 480
 TGAAATGTTT CGTAAGTTAT TGGATTACGC TGAAGCTGGG GACAACGTTG GTACCTTGTT 540
 ACGTGGTGTA ACTCGTGACC AAATCCAACG TGGTCAAGTA TTATCTAAAC CAGGTTCAAT 600
 CACTCCGYAC ACTAAGTTTCG AAGCTGAAGT GTACGTATTG TCTAAAGAAG AAGGTGGTCG 660
 TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC 720
 TGGTGTGTTT ACTTTACCAG AAGGTACTGA AATGGTTATG CCAGGCGACA ACGTACAAAT 780
 GGTTGTTGAA TTGATCCACC CAATCGCGAT CGAAGAA 817

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CTCTGTCAAA TGGGACAAAA ACAGATTTGA AGAAATCATC AAGGAAACCT CCAACTTCGT 60
 CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTTCGT CCAATCTCTG GTTGGAATGG 120
 TGACAACWTG ATTGAASCAT CCACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC 180
 CAAATCCGGT AAAGTTACTG GTAAGACCTT GTTAGAAGCT ATTGACGCTA TTGAACCACC 240
 AACCAGACCA ACCGACAAAC CATTGAGATT GCCATTRCAA GATGTTTACA AGATCGGTGG 300
 TATTGGTACT GTGCCAGTCG GTAGAGTTGA AACTGGTATC ATCAAAGCCG GTATGGTWGT 360
 TACTTTTCGCC CCAGCTGGTG TTACCACTGA AGTCAARTCC GTTGAAATGC ATCACGAACA 420
 ATTGGCTGAA GGTGTTCCAG GTGACAATGT TRGTTTCAAC GTTAAGAACR TTTCCGTTAA 480
 AGAAATTAGA AGAGGTAACG TTTGTGGTGA CTCCAAGAAC GATCCACCAA AGGGTTGTGA 540

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| | |
|---|-----|
| CTCTTTCAAT GCCCAAGTCA TTGTTTTGAA CCATCCAGGT CAAATCTCTG CTGGTTACTC | 600 |
| TCCAGTCTTG GATTGTCACR CTGCCCACAT TGCTTGTAAG TTCGACRCTT TGGTTGAAAA | 660 |
| GATTGACAGA AGAACTGGTA AGRAATTGGA AGAAAATCCA AAATTCGTCA AATCCGGTGA | 720 |
| TGCTGCTATC GTCAAGATGG TCCCAACCAA ACCA | 754 |

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

| | |
|---|-----|
| TCTGTCAAGT GGGATGAATC CAGATTCGCT GAAATCGTTA AGGAAACCTC CAACTTCATC | 60 |
| AAGAAGGTCG GTTACAACCC AAAGACTGTT CCATTCGTCC CAATCTCTGG TTGGAACGGT | 120 |
| GACAACATGA TTGAAGCCAC CACCAACGCT TCCTGGTACA AGGGTTGGGA AAAGGAAACC | 180 |
| AAGGCTGGTG TCGTCAAGGG TAAGACCTTG TTGGAAGCCA TTGACGCTAT CGAACCACCA | 240 |
| ACCAGACCAA CTGACAAGCC ATTGAGATTG CCATTGCAAG ATGTCTACAA GATCGGTGGT | 300 |
| ATCGGTACGG TGCCAGTCGG TAGAGTCGAA ACCGGTGTCA TCAAGCCAGG TATGGTTGTT | 360 |
| ACCTTCGCCC CAGCTGGTGT TACCACTGAA GTCAAGTCCG TTGAAATGCA CCACGAACAA | 420 |
| TTGACTGAAG GTTTGCCAGG TGACAACGTT GGTTTCAACG TTAAGAACGT TTCCGTTAAG | 480 |
| GAAATCAGAA GAGGTAATGT CTGTGGTGAC TCCAAGAACG ACCCACCAAA GGCTGCTGCT | 540 |
| TCTTTCAACG CTACCGTCAT TGTCTTGAAC CACCCAGGTC AAATCTCTGC TGGTTACTCT | 600 |
| CCAGTTTGG ACTGTACAC CGCCACATT GCTTGTAAGT TCGAAGAATT GTTGGAAGAG | 660 |
| AACGACAGAA GATCCGGTAA GAAGTTGGAA GACTCTCCAA AGTTCTTGAA GTCCGGTGAC | 720 |
| GCTGCTTTGG TTAAGTTCGT TCCATCCAAG CCA | 753 |

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

| | |
|---|-----|
| CCGTTAAGTG GGATGAAAAC AGATTTGAAG AAATTGTCAA GGAAACCCAA AACTTCATCA | 60 |
| AGAAGGTTGG TTACAACCCA AAGACTGTTC CATTGTTCC AATCTCTGGT TGAATGGTG | 120 |
| ACAACATGAT TGAAGCATCC ACCAACTGTC CATGGTACAA GGGTTGGACT AAGGAAACCA | 180 |
| AGGCAGGTGT TGTTAAGGGT AAGACCTTAT TAGAAGCAAT CGATGCTATT GAACCACCTG | 240 |
| TCAGACCAAC CGAAAAGCCA TTAAGATTAC CATTACAAGA TGTTTACAAG ATTGGTGGTA | 300 |
| TTGGTACTGT GCCAGTCGGT AGAGTCGAAA CCGGTGTCAT TAAGCCAGGT ATGGTTGTCA | 360 |
| CTTTTGCTCC AGCAGGTGTC ACCACCGAAG TCAAATCCGT TGAAATGCAC CATGAACAAT | 420 |
| TAGAACAAGG TGTTCCAGGT GATAACGTTG GTTCAACGT TAAGAACGTY TCTGTCAAGG | 480 |
| ATATCAAGAG AGGTAACGTT TGTGGTGACT CCAAGAACGA CCCACCAATG GGTGCAGCTT | 540 |
| CTTTCAATGC TCAAGTCATT GTCTTGAACC ACCCTGGTCA AATTTCGCT GGTTACTCTC | 600 |
| CAGTCTTGGA TTGTCACACT GCCCATTG CATGTAAGTT CGACGAATTA ATCGAAAAGA | 660 |
| TTGACAGAAG AACTGGTAAG TCTGTTGAAG ACCATCCAAA GTCYGTCAAG TCTGGTGATG | 720 |
| CAGCTATCGT CAAGATGGTC CCAACCAAGC CA | 752 |

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

| | |
|---|-----|
| CTCAGTCAAA TGGGACAAGA RCAGATACGA AGAAATTGTC AAGGAACTT CCAACTTCGT | 60 |
| CAAGAAGGTT GGTTACAACC CTAAAGCTGT CCCATTCTG CCAATCTCTG GTTGAACGG | 120 |
| TGACAATATG ATTGAACCAT CAACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC | 180 |
| TAAAGCTGGT AAGGTTACCG GTAAGACCTT GTTGAAGCT ATCGATGCTA TCGARCCACC | 240 |

(2) INFORMATION FOR SEQ ID NO: 124:

(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|-----|
| TCTGTTAAAT | GGGACAARAA | CAGATTTGAA | GAAATTATCA | AGGAAACYTC | TAACTTCGTC | 60 |
| AAGAAGGTTG | GTTACAACCC | TAAGGCTGTT | CCATTTCGTT | CAATCTCWGG | TTGGAATGGT | 120 |
| GACAACATGA | TTGAAGCTTC | TACCAACTGT | CCATGGTACA | AGGGTTGGGA | AAAAGAAACC | 180 |
| AAGGCTGGTA | AGGTTACCGG | TAAGACTTTG | TTGGAAGCCA | TTGATGCTAT | TGAACCACCT | 240 |
| TCAAGACCAA | CTGACAAGCC | ATTGAGATTG | CCATTGCAAG | ATGTTTACAA | GATTGGTGGT | 300 |
| ATTGGTACTG | TGCCAGTCGG | TAGAGTTGAA | ACTGGTGTCA | TCAAAGCCGG | TATGGTTGTT | 360 |
| ACTTTYGCCC | CAGCTGGTGT | TACCACTGAA | GTCAAATCCG | TYGAAATGCA | CCACGAACAA | 420 |
| TTGGCTGAAG | GTGTCCCAGG | TGACAATGTT | GGTTTCAACG | TTAAGAACGT | TTCTGTTAAA | 480 |
| GAAATTAGAA | GAGGTAACGT | TTGTGGTGAC | TCCAAGAACG | ATCCACCAAA | GGGTTGTGAC | 540 |
| TCTTTCAACG | CTCAAGTTAT | TGTCTTGAAC | CACCCAGGTC | AAATYTCTGC | TGGTTACTCT | 600 |
| CCAGTCTTGG | ATTGTCACAC | TGCTCATATT | GCTTGTA AAT | TCGACACCTT | GGTTGAAAAG | 660 |
| ATTGACAGAA | GAAGTGGTAA | GAAATTGGAA | GAAAATCCAA | AATTTCGTCAA | ATCCGGTGAT | 720 |

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(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCGCTATC | CTGGTTGTTG | CTGCAACCGA | TGGCCCGATG | CCGCAGACCC | GCGAGCACGT | 60 |
| TCTGCTTGCT | CGCCAGGTTG | GCGTTCCTTA | CATCCTCGTT | GCACTGAACA | AGTGCGACAT | 120 |
| GGTTGATGAT | GAGGAAATCA | TCGAGCTCGT | GGAGATGGAG | ATCTCCGAGC | TGCTCGCAGA | 180 |
| GCAGGACTAC | GATGAGGAAG | CTCCTATCGT | TCACATCTCC | GCTCTGAAGG | CACTCGAGGG | 240 |
| TGACGAGAAG | TGGGTACAGT | CCATCGTTGA | CCTGATGGAT | GCCTGCGACA | ACTCCATCCC | 300 |
| TGATCCGGAG | CGCGCTACCG | ATCAGCCGTT | CTTGATGCCT | ATCGAGGACA | TCTTCACCAT | 360 |
| TACCGGCCGC | GGTACCGTTG | TTACCGGCCG | TGTTGAGCGT | GGTCGTCTGA | ACGTCAACGA | 420 |
| GGACGTTGAG | ATCATCGGTA | TCCAGGAGAA | GTCCCAGAAC | ACCACCGTTA | CCGGTATCGA | 480 |
| GATGTTCCGC | AAGATGATGG | ACTACACCGA | GGCTGGCGAC | AACTGTGGTC | TGCTTCTGCG | 540 |
| TGGTACCAAG | CGTGAGGACG | TTGAGCGTGG | CCAGGTTGTT | ATCAAGCCGG | GCGCTTACAC | 600 |
| CCCTCACACC | AAGTTCGAGG | GTTCCGTCTA | CGTCCTGAAG | AAGGAAGAGG | GCGGCCGCCA | 660 |
| CACCCCGYTC | ATGAACAACT | ACCGTCCTCA | GTTCTACTTC | CGCACCACCG | ACGTTACCGG | 720 |
| TGTTGTGAAC | CTGCCTGAGG | GCACCGAGAT | GGTTATGCCT | GGCGACAACG | TTGAGATGTC | 780 |
| TGTTGAGCTC | ATCCAGCCTG | TTGCTATGGA | CGAG | | | 814 |

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium diphtheriae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

| | |
|--|-----|
| CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCCAATG CCTCAGACCC GTGAGCACGT | 60 |
| TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT GCTCTGAACA AGTGCGACAT | 120 |
| GGTTGATGAT GAGGAAATCA TCGAGCTCGT CGAGATGGAG ATCCRTGAGC TGCTCGCTGA | 180 |
| GCAGGATTAC GACGAAGAGG CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG | 240 |
| CGACGAGAAG TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC | 300 |
| AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA TCTTCACCAT | 360 |
| CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCTCCCTGA AGGTCAACGA | 420 |
| GGACGTCGAG ATCATCGGTA TCCGCGAGAA KGCTACCACC ACCACCGTTA CCGGTATCGA | 480 |
| GATGTTCCGT AAGCTTCTCG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG | 540 |
| TGGCGTTAAG CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC | 600 |
| CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCGTGCC AAGGACGAGG GTGGCCGCCA | 660 |
| CACCCCATTC TTCGACAACT ACCGCCACA GTTCTACTTC CGCACCACCG ACGTTACCGG | 720 |
| TGTTGTGAAG CTTCTGAGG GCACCGAGAT GGTCATGCCT GGCGACAACG TCGACATGTC | 780 |
| CGTCACCCTG ATCCAGCCTG TCGCTATGGA TGAG | 814 |

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

| | |
|---|-----|
| CGGCGCCATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT | 60 |
| TCTGCTGGCT CGCCAGGTTG GCGTTCGTA CATCCTAGTT GCACTGAACA AGTGCGACAT | 120 |
| GGTTGATGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA | 180 |
| GCAGGACTTC GACGAGGAAG CACCTGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG | 240 |
| CGACGAGAAG TGGGCTAAGC AGATCCTGGA GTCATGGAG GCTTGCGACA ACTCCATCCC | 300 |

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GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGRGGACA TCTTCACCAT 360
TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGCCTCCTGA ACCTGAACGA 420
CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG ACCACCGTTA CCTCCATCGA 480
GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCGAC AACGCCGCAC TGCTGCTGCG 540
TGGCCTGAAG CGCGAAGATG TTGAGCGTGG TCAGATCGTT GCTAAGCCGG GCGAGTACAC 600
CCCGCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA 660
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTATTTC CGCACCACCG ACGTTACCGG 720
TGTTGTGAAG CTGCCGGAGG GCACCGAGAT GGTTATGCCG GCGACAACG TTGACATGTC 780
CGTCACCCTG ATCCAGCCGG TTGCTATGGA CGAG 814

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CGGCGCCATC CTGGTTGTTG CCGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT 60
TCTGCTGGCY CGCCAGGTTG GCGTTCCGTA CATCCTGGTT GCACTGAACA AGTGTGACAT 120
GGTTGACGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA 180
GCAGGACTTC GACGAGGAAG CTCCGGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG 240
CGACGAGAAG TGGGCTAACC AGATTCTCGA GCTGATGCAG GCTTGCGACG AGTCTATCCC 300
GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGWGGACA TCTTCACCAT 360
TACCGGTCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGCATCCTGA ACCTGAACGA 420
CGAGGTTGAG ATCCTGGGTA TCCGCGAGAA GTCCCAGAAG ACCACCGTTA CCTCCATCGA 480
GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCRAC AACGCTGCAC TGCTGCTGCG 540
TGGTCTGAAG CGCGAGGACG TTGAGCGTGG CCAGATCATC GCTAAGCCGG GCGAGTACAC 600
CCCGCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GCGGCCGCCA 660
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGCACCACCG ACGTTACCGG 720

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(2) INFORMATION FOR SEQ ID NO: 129:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

(2) INFORMATION FOR SEQ ID NO: 130:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium striatum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

| | |
|---|-----|
| GGCGCTATCT TGGTTGTTGC TGCAACCGAT GGCCCGRTGC CGCAGACCCG CGAGCACGTT | 60 |
| CTTCTGGCTC GCCAGGTTGG CGTTCCTTAC ATCCTCGTTG CACTGAACAA GTGCGACATG | 120 |
| GTTGACGACG AGGAAATTAT CGAGCTCGTC GAGATGGAGA TCCGCGAACT GCTCGCAGAG | 180 |
| CAGGACTACG ATGAGGAAGC TCCGATCGTT CACATCTCTG CTCTGAAGGC TCTTGAGGGC | 240 |
| GRCGAGAAGT GGGTACAGGC TATCGTTGAC CTGATGCAGG CTTGCGATGA CTCCATCCCG | 300 |
| GATCCGGAGC GCGAGCTGGA CAAGCCGTTT CTGATGCCAA TCGAGGACAT CTTACCATC | 360 |
| ACCGGCCGCG GTACCGTTGT TACTGGCCGT GTTGAGCGTG GCTCCCTGAA CGTCAACGAG | 420 |
| GACGTTGAGA TCATCGGTAT CCAGGACARG TCCATCTCCA CCACCGTTAC CGGTATCGAG | 480 |
| ATGYTCCGCA AGATGATGGA CTACACCGAG GCTGGCGACA ACTGTGGTCT GCTTCTGCGT | 540 |
| GGTACCAAGC GTGAAGAGGT TGAGCGCGGC CAGGTTGTTA TTAAGCCGGG CGCTTACACC | 600 |
| CCTCACACCC AGTTCGAGGG TTCCGTCTAC GTCCTGAAGA AGGAAGAGGG CGGCCGCCAC | 660 |
| ACCCCGTTCA TGGACAACTA CCGTCCGCAG TTCTACTTCC GCACCACCGA CGTTACCGGC | 720 |
| GTCATCAAGC TGCCTGAGGG CACCGAGATG GTTATGCCTG GCGACAACGT CGAGATGTCY | 780 |
| GTCGAGCTGA TCCAGCCGGT CGCTATGGAC GAG | 813 |

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus avium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

| | |
|---|-----|
| CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAATC GTGAACACAT | 60 |
| CTTGTTATCT CGTAACGTTG GTGTTCTTA CATCGTTGTA TTCTTAAACA AAATGGATAT | 120 |
| GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA GTTCGTGACT TATTAAGTGA | 180 |
| ATACGACTTC CCAGGCGACG AACTCCAGT TATCGCAGGT TCAGCGTTGA AAGCTTTAGA | 240 |
| AGGCGACGCT TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATATAT | 300 |

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| | |
|--|-----|
| CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC | 360 |
| AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA CGTGGACAAG TTCGCGTTGG | 420 |
| TGACGAAGTT GAAATCGTAG GTATCGCTGA CGAAACTGCT AAAACAACCTG TTACAGGTGT | 480 |
| TGAAATGTTC CGTAAATTGT TAGACTACGC TGAAGCAGGT GACAACATCG GTGCTTTGTT | 540 |
| ACGTGGTGTT GCACGTGAAG ATATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT | 600 |
| CACTCCACAT ACAAATTCT CTGCAGAAGT TTATGTTCTA ACTAAAGAAG AAGGTGGACG | 660 |
| TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC | 720 |
| TGGTGTAGTT GATCTACCAG AAGGTACTGA AATGGTWATG CCTGGGGATA ACGTAACTAT | 780 |
| GGAAGTTGAA TTGATYCACC CAATYCGCGT AGAAGAC | 817 |

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

| | |
|---|-----|
| CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACAC GTGAACATAT | 60 |
| CTTATTATCA CGTAACGTTG GTGTACCATA CATCGTTGTA TTCTTAAACA AAATGGATAT | 120 |
| GGTTGATGAC GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA | 180 |
| ATACGATTC CCAGGCGATG ATGTTCCAGT TATCGCAGGT TCTGCTTTGA AAGCTTTAGA | 240 |
| AGGCGACGAG TCTTATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT | 300 |
| CCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC | 360 |
| AATCACTGGA CGTGGTACTG TTGCTACAGG ACGTGTGAA CGTGGTGAAG TTCGCGTTGG | 420 |
| TGACGAAGTT GAAATCGTTG GTATTAAAGA CGAAACATCT AAAACAACYG TTACAGGTGT | 480 |
| TGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCAGGC GACAACMTCG GTGCTTTATT | 540 |
| ACGTGGTGTA GCACGTGAAG ATATCGAACG TGGACAAGTA TTAGCTAAAC CAGCTACAAT | 600 |
| CACTCCACAC ACAAATTCA AAGCTGAAGT ATACGTATTA TCAAAAGAAG AAGGCGGACG | 660 |
| TCACACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACGTTAC | 720 |

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TGGTGTGTTGTA GAATTGCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACGTTGCTAT 780
GGACGTTGAA TTAATTCACC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 774 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGGAGCTATC TTGGTAGTTT CTGCTGCTGA CGGCCCAATG CCTCAAACCTC GTGAACACAT 60
CCTATTGTCT CGTCAAGTTG GTGTTCTTA CATCGTTGTA TTCTTGAACA AAGTAGACAT 120
GGTTGATGAC GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA 180
ATACRAATTC CCTGGTGRCG ATGTTCTGT AGTTGCTGGA TCAGCTTTGA AAGCTCTAGA 240
AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG GCTGCAGTTG ACGAATACAT 300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTCTC 360
AATTACTGGA CGTGGTACTG TTGCTACAGG TCGTGTGAA CGTGGACAAG TTCGCGTTGG 420
TGACGAAGTT GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTACTGGTGT 480
TGAAATGTTC CGTAAATTGT TAGACYACGC TGAAGCTGGA GACRACATTG GTGCTTTACT 540
ACGTGGTGTT GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT 600
CACACCTCRT ACAAATTCT CTGCAGAAGT ATACGTGTTG ACAAAGAAG AAGGTGGACG 660
TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC 720
AGGTGTTGTT GAATTACCAG AAGGAACTGA AATGGTCATG CCCGGTGACA ACGT 774

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 809 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Enterococcus gallinarum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

| | |
|--|-----|
| CGGTGCGATC TTAGTAGTAT CTGCTGCTGA CGGTCCTATG CCTCAAACCTC GTGAACACAT | 60 |
| CTTGTTATCA CGTAACGTTG GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT | 120 |
| GGTTGAYGAC GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA | 180 |
| ATATGACTTC CCAGGCGACG ATGTTCTGT AATCGCCGGT TCTGCTTTGA AAGCTCTTGA | 240 |
| AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG GCTGCAGTTG ACGAATACGT | 300 |
| TCCAACCTCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC | 360 |
| AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTGAA CGTGGACAAG TTCGCGTTGG | 420 |
| TGATGAAGTA GAAATCGTTG GTATTGCTGA CGAACTGCT AAAACAACTG TAACAGGTGT | 480 |
| TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT | 540 |
| ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT | 600 |
| CACACCTCAT ACAAATTCA AAGCTGAAGT TTATGTTTTG ACAAAGAAG AAGGTGGACG | 660 |
| TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC | 720 |
| TGGTGTGTT GAATTACCAG AAGGAACTGA AATGGTGATG CCTGGCGACA ACGTGACCAT | 780 |
| CGACGTTGAA TTGATRCACC CAATCGCTC | 809 |

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gardnerella vaginalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

| | |
|--|-----|
| TGGCGCAATC CTCGTGGTTG CTGCTACCGA CGGTCCAATG GCTCAGACCC GTGAACACGT | 60 |
| CTTGCTTGCT AAGCAGGTCG GCGTTCCAAA AATTCTTGTT GCTTTGAACA AGTGCGATAT | 120 |
| GGTTGACGAC GAAGAGCTTA TCGATCTCGT TGAAGAAGAG GTCCGTGACC TCCTCGAAGA | 180 |
| AAACGGCTTC GATCGCGATT GCCCAGTCYT CCGTACTTCC GCTTACGGCG CTTTGCATGA | 240 |
| TGACGCTCCA GACCACGACA AGTGGGTTAGA GACCGTCAAG GAACTCATGA AGGCTGTTGA | 300 |

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| | |
|---|-----|
| CGAGTACATC CCAACCCCAA CTCACGATCT TGACAAGCCA TTCTTGATGC CAATCGAAGA | 360 |
| TGTGTTTACC ATCTCCGGTC GTGGTYCCGT TGTCACCGGT CGTGTTGAGC GTGGTAAGCT | 420 |
| CCCAATCAAC ACCCCAGTTG AGATCGTTGG TTTGCGCGAT ACCCAGACCA CCACCGTCAC | 480 |
| CTCTATCGAG ACCTTCCACA AGCAGATGGA TGAGGCAGAG GCTGGCGATA AACTGGTCT | 540 |
| TCTTCTCCGC GGTATCAACC GTACCGACGT TGAGCGTGGT CAGGTTGTGG CTGCTCCAGG | 600 |
| TTCTGTGACT CCACACACCA AGTTCGAAGG CGAAGTTTAC GTCTTGACCA AGGACGAAGG | 660 |
| TGGCCGTCAC TCGCCATTCT TCTCCAATA CCGTCCACAG TTCTACTTCC GTACCACCGA | 720 |
| TGTTACTGGC GTTATCACCT TGCCAGACGG CATCGAAATG GTTCAGCCAG GCGATCACGC | 780 |
| AACCTTCACT GTTGAGTTGA TCCAGGCTAT CGCAATGGAA GAG | 823 |

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria innocua*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

| | |
|--|-----|
| CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAACTC GTGAACATAT | 60 |
| CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT | 120 |
| GGTTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA | 180 |
| ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA | 240 |
| AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT | 300 |
| TCCAACCTCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC | 360 |
| AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG | 420 |
| TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAA AAAGTAGTAG TAACTGGAGT | 480 |
| AGAAATGTTC CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT | 540 |
| ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT | 600 |
| TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG | 660 |
| TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC | 720 |

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TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT 780
 TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria ivanovii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC GTGAACATAT 60
 TCTTACTTTC ACGTCAAGTT GGTGTTCCAT ACATCGTTGT ATTCATGAAC AAATGTGACA 120
 TGGTTGACGA TGAAGAATTA CTTGAATTAG TTGAAATGGA AATTCGTGAT CTATTAAGT 180
 AATATGAATT CCCTGGCGAC GACATTCCTG TAATCAAAGG TTCAGCTCTT AAAGCACTTC 240
 AAGGTGAAGC TGATTGGGAA GCTAAAATTG ACGAGTTAAT GGAAGCTGTA GATTCTTACA 300
 TTCCAAGTCC AGAACGTGAT ACTGACAAAC CATTGATGAT GCCAGTTGAG GATGTATTCT 360
 CAATCACTGG TCGTGGAACA GTTGCAACTG GACGTGTTGA ACGTGGACAA GTTAAAGTTG 420
 GTGACGAAGT AGAAGTTATC GGTATTGAAG AAGAAAGCAA AAAAGTAGTA GTAAGTGGAG 480
 TAGAAATGTT CCGTAAATTA CTAGACTACG CTGAAGCTGG CGACAACATT GGCGCACTTC 540
 TACGTGGTGT TGCTCGTGAA GATATCCAAC GTGGTCAAGT ATTAGCTAAA CCAGGTTCTGA 600
 TTACTCCACA TACTAACTTC AAAGCTGAAA CTTATGTTTT AACTAAAGAA GAAGGTGGAC 660
 GTCATACTCC ATTCTTCAAC AACTACCGCC CACAATTCTA TTTCCGTACT ACTGACGTAA 720
 CTGGTATTGT TACACTTCCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACATTGAGC 780
 TTGCAGTTGA ACTAATTGCA CCAATCGCTA TCGAAGAC 818

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 817 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

| | |
|--|-----|
| CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT | 60 |
| CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT | 120 |
| GGTTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA | 180 |
| ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA | 240 |
| AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT | 300 |
| TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC | 360 |
| AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTGAA CGTGGACAAG TTAAAGTTGG | 420 |
| TGACGAAGTA GAAGTTATCG GTATCGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT | 480 |
| AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT | 540 |
| ACGTGGTGTT GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT | 600 |
| TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG | 660 |
| TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC | 720 |
| TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAAYG CCTGGTGATA ACATTGAGCT | 780 |
| TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC | 817 |

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria seeligeri*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

| | |
|---|-----|
| CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT | 60 |
| CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT | 120 |
| GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA | 180 |
| ATATGAATTC CCTGGTGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA | 240 |

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AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
TCCAACCTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC 360
AATCACTGGT CGTGGAAGCTG TTGCAACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG 420
TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAATAG TAACTGGAGT 480
AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT 540
ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT 600
TACTCCACAT ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG 660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC 720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT 780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CGGTGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC GTGAACACAT 60
TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA TTCTTAAACA AAGTTGACAT 120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTAAGCGA 180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCAGCATTAR AAGCTTTAGA 240
AGGCGATGCT CAATACGAAG AAAAAATCTT AGAATTARTG GAAGCTGTAG ATACTTACAT 300
TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC 360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTTGG 420
TGAAGAAGTT GAAATCATCG GTTTACATGA CACATCTAAA ACAACTGTTA CAGGTGTTGA 480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG 540
TGGTGTTGCT CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG GTGGACGTCA 660

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(2) INFORMATION FOR SEQ ID NO: 141:

(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

(2) INFORMATION FOR SEQ ID NO: 142:

(A) LENGTH: 817 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CGGAGCTATC | TTAGTAGTAT | CTGCTGCTGA | TGGCCCAATG | CCACAAACTC | GTGAACACAT | 60 |
| TCTTTTATCA | CGTRACGTTG | GTGYTCCAGC | ATTAGTTGTA | TTCTTAAACA | AAGTTGACAT | 120 |
| GGTTGACGAY | GAAGAATTAT | TAGAATTRGT | AGAAATGGAA | GTTCGTGRCT | TATTAAGCGA | 180 |
| ATATGACTTC | CCAGGTGACG | ATGTACCTGT | AATCTCTGGT | TCTGCATTAA | AAGCTTTAGA | 240 |
| AGGCGACGCT | GACTATGAGC | AAAAAATCTT | AGACTTAATG | CAAGCTGTTG | ATGACTYCAT | 300 |
| TCCAACACCA | GAACGTGATT | CTGACAAACC | ATTGATGATG | CCAGTTGAGG | ACGTATTCTC | 360 |
| AATCACTGGT | CGTGGTACTG | TTGCTACAGG | CCGTGTTGAA | CGTGGTCAAA | TCAAAGTCGG | 420 |
| TGAAGAAATC | GARATCATCG | GTATGCAAGA | AGAATCAAGC | AAAACAACCTG | TTACTGGTGT | 480 |
| AGAAATGTTC | CGTAAATTAT | TAGACTACGC | TGAAGCTGGT | GACAACATTG | GTGCATTATT | 540 |
| ACGTGGTGTT | TCACGTGATG | ATGTACAACG | TGGTCAAGTT | TTAGCTGCTC | CTGGTACTAT | 600 |
| CACACCACAT | ACAAAATTCA | AAGCGGATGT | TTACGTTTTA | TCTAAAGATG | AAGGTGGTCG | 660 |
| TCATACGCCA | TTCTTCACTA | ACTACCGCCC | ACAATTCTAT | TTCCGTACTA | CTGACGTAAC | 720 |
| TGGTGTTGTT | AACTTACCAG | AAGGTACTGA | AATGGTTATG | CCTGGCGATA | ACGTTGAAAT | 780 |
| GGATGTTGAA | TTAATTTCTC | CAATCGCTAT | TGAAGAC | | | 817 |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CGGCGGTATC | TTAGTAGTAT | CTGCTGCAGA | TGGTCCAATG | CCACAAACTC | GTGAACACAT | 60 |
| CTTATTATCA | CGTAACGTTG | GTGTACCAGC | TTTAGTTGTA | TTCTTAAACA | AAGCTGACAT | 120 |
| GTTTGACGAC | GAAGAATTAT | TAGAATTAGT | TGAAATGGAA | GTTCTGTGACT | TATTATCTGA | 180 |

ATACGACTTC CCTGGTGACG ATGTACCAGT TATCGTTGGT TCTGCATTAA AAGCTTTAGA 240
 AGGCGACCCA GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCTGTAG ATGACTACAT 300
 CCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC 360
 AATCACTGGT CGTGGTACTG TAGCAACAGG CCGTGTGAA CGTGGTCAA TCAAAGTCGG 420
 TGAAGAAGTT GAAATCATCG GTATCACTGA AGAAAGCAAG AAAACAACAG TTACAGGTGT 480
 AGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT 540
 ACGTGGTGTT GCACGTGAAG ACGTACAACG TGGACAAGTA TTAGCAGCTC CTGGCTCTAT 600
 TACTCCACAC AAAAAATTCA AAGCTGATGT TTACGTTTTA TCTAAAGAAG AAGGTGGACG 660
 TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC TTCCGTACTA CTGACGTAAC 720
 TGGCGTTGTT CACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTAGAAAT 780
 GACTGTTGAA TTGATCGCTC CAATCGCGAT TGAAGAC 817

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC GTGAGCACAT 60
 CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA TTCATGAACA AAGTTGACCT 120
 TGTTGATGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATTCGTGACC TTCTTTCAGA 180
 ATACGACTTC CCAGGTGATG ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA 240
 AGGCGACGAA AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT 300
 TCCAGAACCA GAACGTGATA CTGACAAAACC TTTACTTCTT CCAGTTGAAG ATGTATTCTC 360
 AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTACTG TTCGTGTCAA 420
 CGACGAAGTT GAAATCGTTG GTATTAAAGA AGATATCCAA AAAGCAGTTG TTACTGGTGT 480
 TGAAATGTTC CGTAAACAAC TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT 540
 TCGTGGTGTT CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600

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| | |
|---|-----|
| CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG | 660 |
| TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC | 720 |
| AGGTTCAATC GAACTTCCAG CAGGAACAGA AATGGTTATG CCTGGTGATA ACGTTACTAT | 780 |
| CGAAGTTGAA TTGATTCACC CAATCGCCGT AGAACAA | 817 |

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

| | |
|---|-----|
| CGGAGCTATC CTTGTAGTAG CTTCAACTGA CGGACCAATG CCACAAACTC GTGAGCACAT | 60 |
| CCTTCTTTCA CGTCAGGTTG GTGTTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT | 120 |
| GGTTGACGAC GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TATTGTCAGA | 180 |
| ATACGACTTC CCAGGTGACG ATCTTCCAGT TATCCAAGGT TCAGCACTTA AAGCTCTTGA | 240 |
| AGGTGACTCT AAATACGAAG ACATCGTTAT GGAATTGATG AACACAGTTG ATGAGTATAT | 300 |
| CCCAGAACCA GAACGTGACA CTGACAAACC ATTGCTTCTT CCAGTCGAGG ACGTATTCTC | 360 |
| AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTATCG TTAAAGTCAA | 420 |
| CGACGAAATC GAAATCGTTG GTATCAAAGA AGAACTCRA AAAGCAGTTG TTACTGGTGT | 480 |
| TGAAATGTTT CGTAAACAAC TTGACGAAGG TCTTGCTGGA GATAACGTAG GTGTCCTTCT | 540 |
| TCGTGGTGTT CAACGTGATG AAATCGAAGC TGGACAAGTT ATCGCTAAAC CAGGTTCAAT | 600 |
| CAACCCACAC ACTAAATTTA AAGGTGAAGT CTACATCCTT ACTAAAGAAG AAGGTGGACG | 660 |
| TCACACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACTA CTGACGTTAC | 720 |
| AGGTTCAATC GAACTTCCAG CAGGTACTGA AATGGTAATG CCTGGTGATA ACGTGACAAT | 780 |
| CGACGTTGAG TTGATTCACC CAATCGCCGT AGAACAA | 817 |

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus salivarius*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

| | |
|---|-----|
| CGGTGCGATC CTTGTAGTAG CATCTACTGA CGGACCAATG CCACAAACTC GTGAGCACAT | 60 |
| CCTTCTTTCA CGTCAGGTTG GTGTTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT | 120 |
| GGTTGACGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TTCTTTCAGA | 180 |
| ATACGATTTC CCAGGTGATG ACATTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA | 240 |
| AGGTGATTCT AAATACGAAG ACATCATCAT GGACTTGATG AACACTGTTG ACGAATACAT | 300 |
| CCCAGAACCA GAACGTGACA CTGACAAACC ATTGTTGCTT CCAGTCGAAG ACGTATTCTC | 360 |
| AATCACTGGT CGTGGTACTG TTGCTTCAGG ACGTATCGAC CGTGGTGTTG TTCGTGTCAA | 420 |
| TGACGAAGTT GAAATCGTTG GTCTTAAAGA AGACATCCAA AAAGCAGTTG TTACTGGTGT | 480 |
| TGAAATGTTT CGTAAACAAC TTGACGRAGG TATTGCCGGA GATAACGTCG GTGTTCTTCT | 540 |
| TCGTGGTATC CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTGCAC CTGGTTCAAT | 600 |
| CAACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG | 660 |
| TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC TTCCGTACAA CTGACGTAAC | 720 |
| AGGTTCAATC GAACTTCCTG CAGGTACTGA AATGGTTATG CCTGGTGATA ACGTGACTAT | 780 |
| CGACGTTGAG TTGATCCACC CAATCGCCGT TGAACAA | 817 |

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Agrobacterium tumefaciens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

| | |
|---|-----|
| AACATGATCA CCGGTGCTGC CGAGATGGAC GGCGCGATCC TGGTTTGCTC GGCTGCCGAC | 60 |
| GGCCCGATGC CACAGACCCG CGAGCACATC CTGCTTGCCC GTCAGGTGGG CGTTCCGGCC | 120 |

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| | |
|--|-----|
| ATCGTCGTGT TCCTCAACAA GGTCGACCAG GTTGACGACG CCGAGCTTCT CGAGCTCGTC | 180 |
| GAGCTTGAAG TTCGCGAACT TCTGTCGTCC TACGACTTCC CGGGCGACGA TATCCCCGATC | 240 |
| ATCAAGGGTT CGGCACTTGC TGCTCTTGAA GATTCTGACA AGAAGATCGG TGAAGACGCG | 300 |
| ATCCGCGAGC TGATGGCTGC TGTCGACGCC TACATCCCCG CGCCTGAGCG TCCGATCGAC | 360 |
| CAGCCGTTCC TGATGCCGAT CGAAGACGTG TTCTCGATCT CGGGTCGTGG TACGGTTGTG | 420 |
| ACGGGTCGCG TTGAGCGCGG TATCGTCAAG GTTGGTGAAG AAGTCGAAAT CGTCGGCATC | 480 |
| CGTCCGACCT CGAAGACGAC TGTTACCGGC GTTGAAATGT TCCGCAAGCT GCTCGACCAG | 540 |
| GGCCAGGCCG GCGACAACAT CGGTGCACTC GTTCGCGGCG TTACCCGTGA CGGCGTCGAG | 600 |
| CGTGGTCAGA TCCTGTGCAA GCCGGGTTTC GTCAAGCCGC ACAAGAAGTT CATGGCAGAA | 660 |
| GCCTACATCC TGACGAAGGA AGAAGGCGGC CGTCATACGC CGTTCTTCAC GAACTACCGT | 720 |
| CCGCAGTTCT ACTTCCGTAC GACTGACGTT ACCGGTATCG TTTCGCTTCC TGAAGGCACG | 780 |
| GAAATGGTTA TGCCTGGCGA CAACGTCACT GTTGAAGTCG AGCTGATCGT TCCGATCGCG | 840 |
| ATGGAAGAAA AGCTGCGCTT CGCTATCCGC GAAGGCGGCC GTACCGTCGG CGCCGGC | 897 |

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

| | |
|---|-----|
| ATGATCACTG GTGCTGCGCA AATGGACGGA GCTATCCTTG TAGTATCTGC TGCTGATGGC | 60 |
| CCAATGCCAC AAACCTCGTA GCACATCCTT CTTTCTAAAA ACGTTGGTGT ACCATACATC | 120 |
| GTTGTATTCT TAAACAAATG CGACATGGTA GACGACGAAG AGCTTCTTGA ACTAGTTGAA | 180 |
| ATGGAAGTTC GCGATCTTCT TAGCGAATAC GACTTCCCTG GTGATGATGT ACCAGTTGTT | 240 |
| AAAGGTTCTG CTCTTAAAGC TCTTGAAGGA GACGCTGAGT GGGAAGCTAA AATCTTCGAA | 300 |
| CTTATGGATG CGGTTGATGA GTACATCCCA ACTCCAGAAC GCGACACTGA AAAACCATTC | 360 |
| ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACAGTTGC TACTGGCCGT | 420 |
| GTAGAACGCG GACAAGTTAA AGTCGGTGAC GAAGTTGAAA TCATCGGTCT TCAAGAAGAG | 480 |

| | |
|---|-----|
| AACAAGAAAA CAACTGTTAC AGGTGTTGAA ATGTTCCGTA AGCTTCTTGA TTACGCTGAA | 540 |
| GCTGGTGACA ACATTGGTGC CCTTCTTCGC GGTGTATCTC GTGAAGAAAT CCAACGTGGT | 600 |
| CAAGTACTTG CTAAACCAGG TACAATCACT CCACACAGCA AATTCAAAGC TGAAGTTTAC | 660 |
| GTTCTTTCTA AAGAAGAGGG TGGACGTCAT ACTCCATTCT TCTCTAACTA CCGTCCTCAG | 720 |
| TTCTACTTCC GTACAACTGA CGTAACTGGT ATCATCCATC TTCCAGAAGG CGTAGAAATG | 780 |
| GTTATGCCTG GAGATAACAC TGAAATGAAC GTTGAACTTA TTTCTACAAT CGCTATCGAA | 840 |
| GAAGGAACTC GTTTCTCTAT TCGTGAAGGC GGACGTACTG TTGGT | 885 |

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

| | |
|--|-----|
| ATGGTTACTG GTGCTGCTCA GATGGACGGT GCTATCATTG TAGTTGCTGC TACTGATGGT | 60 |
| CCGATGCCTC AGACTCGTGA GCACATCCTT TTGGCTCGTC AGGTAAACGT TCCGAAGCTG | 120 |
| GTTGTATTCA TGAACAAGTG CGATATGGTT GAAGATGCTG AGATGTTGGA ACTTGTTGAA | 180 |
| ATGGAAATGA GAGAATTGCT TTCATTCTAT GATTTTCGACG GTGACAATAC TCCGATCATT | 240 |
| CAGGGTTCTG CTCTTGGTGC ATTGAACGGC GTAGAAAAAT GGGAAGACAA AGTAATGGAA | 300 |
| CTGATGGAAG CTGTTGATAC TTGGATTCCA CTGCCTCCGC GCGATGTTGA TAAACCTTTC | 360 |
| TTGATGCCGG TAGAAGACGT GTTCTCTATC ACAGGTCGTG GTACTGTAGC TACAGGTCGT | 420 |
| ATCGAAACTG GTGTTATCCA TGTAGGTGAT GAAATCGAAA TCCTCGGTTT GGGTGAAGAT | 480 |
| AAGAAATCAG TTGTAACAGG TGTGAAATG TTCCGCAAAC TTCTGGATCA GGGTGAAGCT | 540 |
| GGTGACAACG TAGGTCTGTT GCTTCGTGGT GTTGACAAGA ACGAAATCAA ACGTGGTATG | 600 |
| GTTCTTTGTA AACC GGGTCA GATTAAACCT CACTCTAAAT TCAAAGCAGA GGTTTATATC | 660 |
| CTGAAGAAAG AAGAAGGTGG TCGTCACACT CCATTCCATA ACAAATATCG TCCTCAGTTC | 720 |
| TACCTGCGTA CTATGGACTG TACAGGTGAA ATCACTCTTC CGGAAGGAAC TGAAATGGTA | 780 |
| ATGCCGGGTG ATAACGTAAC TATCACTGTA GAGTTGATCT ATCCGGTTGC ACTGAACATC | 840 |

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GGTCTTCGTT TCGCTATCCG CGAAGGTGGA CGTACAGTAG GT

882

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

| | |
|---|-----|
| AATATGATTA CAGGAGCAGC TCAAATGGAT GCAGCGATAC TTTTAGTTGC TGCTGATAGT | 60 |
| GGTGCTGAGC CTCAAACAAA AGAGCATTTG CTTCTTGCTC AAAGAATGGG AATAAAGAAA | 120 |
| ATAATAGTTT TTTTAAATAA ATTGGACTTA GCAGATCCTG AACTTGTTGA GCTTGTTGAA | 180 |
| GTTGAAGTTT TAGAACTTGT TGAAAAATAT GGCTTTTCAG CTGATACTCC AATAATCAAA | 240 |
| GGTTCAGCTT TTGGGGCTAT GTCAAATCCA GAAGATCCTG AATCTACAAA ATGCGTTAAA | 300 |
| GAAGTTCTTG AATCTATGGA TAATTATTTT GATCTTCCAG AAAGAGATAT TGACAAGCCA | 360 |
| TTTTTGCTTG CTGTTGAAGA TGTATTTTCT ATTTTCAGGAA GAGGCACTGT TGCTACTGGG | 420 |
| CGTATTGAAA GAGGTATTAT TAAAGTTGGT CAAGAAGTTG AAATAGTTGG AATTAAAGAA | 480 |
| ACCAGAAAAA CTAAGTTTAC TGGTGTGTTGAA ATGTTCCAGA AAATTCTTGA GCAAGGTCAA | 540 |
| GCAGGGGATA ATGTTGGTCT TCTTTTGAGA GCGGTTGATA AAAAAGACAT TGAGAGGGGG | 600 |
| CAAGTTTTGT CAGCTCCAGG TACAATTACT CCACACAAGA AATTTAAAGC TTCAATTTAT | 660 |
| TGTTTGACTA AAGAAGAAGG CGGTAGGCAC AAGCCATTTT TCCCAGGGTA TAGACCACAG | 720 |
| TTCTTTTTTA GAACAACCGA TGTTACTGGA GTTGTTGCTT TAGAGGGCAA AGAAATGGTT | 780 |
| ATGCCTGGTG ATAATGTTGA TATTATTGTT GAGCTGATCT CTTCAATAGC TATGGATAAG | 840 |
| AATGTAGAAT TTGCTGTTTCG AGAAGGTGGA AGAACCGTTG CTTTCAGGA | 888 |

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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100211-14001

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Brevibacterium linens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AACATGATCA | CCGGTGCCGC | TCAGATGGAC | GGTGCGATCC | TCGTGTCGC | CGCTACCGAC | 60 |
| GGACCGATGC | CCCAGACCCG | TGAGCACGTG | CTGCTCGCGC | GTCAGGTCGG | CGTTCCCTAC | 120 |
| ATCGTCGTGG | CTCTGAACAA | GTCCGACATG | GTCGATGACG | AGGAGCTCCT | CGAGCTCGTC | 180 |
| GAATTCGAGG | TCCGCGACCT | GCTCTCGAGC | CAGGACTTCG | ACGGAGACAA | CGCTCCGGTC | 240 |
| ATTCCGGTGT | CCGCTCTCAA | GGCGCTGGAA | GGCGACGAGA | AGTGGGTCAA | GAGCGTTCAG | 300 |
| GATCTCATGG | CTGCCGTCGA | TGACAACGTT | CCGGAGCCGG | AGCGCGATGT | CGACAAGCCG | 360 |
| TTCTTCATGC | CCGTCGAGGA | CGTCTTCACG | ATCACCGGTC | GTGGAACCGT | CGTCACCGGT | 420 |
| CGTGTCGAGC | GCGGCGTGCT | CCTGCCTAAC | GACGAAATCG | AAATCGTCGG | CATCAAGGAG | 480 |
| AAGTCGTCCA | AGACGACTGT | CACCGCTATC | GAGATGTTCC | GCAAGACCTT | GCCGGATGCC | 540 |
| CGTGCAGGTG | AGAACGTCGG | TCTGCTCCTC | CGCGGCACCA | AGCGCGAGGA | TGTTGAGCGC | 600 |
| GGTCAGGTCA | TCGTGAAGCC | GGGTTCGATC | ACCCCGCACA | CCAAGTTCGA | GGCTCAGGTC | 660 |
| TACATCCTGA | GCAAGGACGA | GGGCGGACGT | CACAACCCGT | TCTACTCGAA | CTACCGTCCG | 720 |
| CAGTTCTACT | TCCGGACCAC | GGACGTCACC | GGTGTCATCA | CGCTGCCCCG | GGGCACCGAG | 780 |
| ATGGTCATGC | CCGGCGACAA | CACCGATATG | TCGGTCGAGC | TCATCCAGCC | GATCGCTATG | 840 |
| GAGGACCGCC | TCCGCTTCGC | AATCCGCGAA | GGTGGCCGCA | CCGTGCGCGC | CGGT | 894 |

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| ATGATCACGG | GCGCAGCGCA | GATGGACGGC | GCGATCCTGG | TTTGCTCGGC | AGCAGACGGC | 60 |
| CCGATGCCGC | AAACGCGTGA | GCACATCCTG | CTGGCGCGTC | AGGTTGGTGT | TCCGTACATC | 120 |
| ATCGTGTTC | TGAACAAGTG | CGACAGTGTG | GACGACGCTG | AACTGCTCGA | GCTGGTTCGAG | 180 |

ATGGAAGTTC GCGAACTCCT GTCGAAGTAC GACTTCCCGG GCGACGACAC GCCGATCGTG 240
AAGGGTTCGG CCAAGCTGGC GCTGGAAGGC GACACGGGCG AGCTGGGCGA AGTGGCGATC 300
ATGAGCCTGG CAGACGCGCT GGACACGTAC ATCCCGACGC CGGAGCGTGC AGTTGACGGC 360
GCGTTCCTGA TGCCGGTGGG AGACGTGTTC TCGATCTCGG GCCGTGGTAC GGTGGTGACG 420
GGTCGTGTCG AGCGCGGCAT CGTGAAGGTC GGCGAAGAAA TCGAAATCGT CCGTATCAAG 480
CCGACGGTGA AGACGACCTG CACGGGCGTT GAAATGTTCC GCAAGCTGCT GGACCAAGGT 540
CAGGCAGGCG ACAACGTCGG TATCCTGCTG CGCGGCACGA AGCGTGAAGA CGTGAGCGT 600
GGCCAGGTTC TGGCGAAGCC GGGTTCGATC ACGCCGCACA CGCACTTCAC GGCTGAAGTG 660
TACGTGCTGA GCAAGGACGA AGGCGGCCGT CACACGCCGT TCTTCAACAA CTACCGTCCG 720
CAGTTCTACT TCCGTACGAC GGACGTGACG GGCTCGATCG AGCTGCCGAA GGACAAGGAA 780
ATGGTGATGC CGGGCGACAA CGTGTGATC ACGGTGAAGC TGATTGCTCC GATCGCGATG 840
GAAGAAGGTC TGCGCTTCGC AATCCGTGAA GGCGGCCGTA CCGTCGGC 888

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

AACATGATCA CCGGTGCGGC TCAAATGGAC GGGGCTATTC TAGTAGTTTC TGCAACAGAC 60
GGAGCTATGC CTCAAATAA AGAGCATATT CTTTGGCAA GACAAGTTGG GGTTCCTTAC 120
ATCGTTGTTT TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC 180
TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG GTGTCCAATC 240
ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGAGATGCTG CATACATAGA GAAAGTTCGA 300
GAGCTAATGC AAGCCGTCGA TGATAATATC CCTACTCCAG AAAGAGAAAT TGACAAGCCT 360
TTCTTAATGC CTATTGAGGA CGTGTCTCT ATCTCCGAC GAGGAACTGT AGTAACTGGA 420
CGTATTGAGC GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT 480
ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAGAA AAGAACTCCC AGAAGGTCGT 540

| | |
|---|-----|
| GCAGGAGAGA ACGTTGGATT GCTCCTCAGA GGTATTGGTA AGAACGATGT GGAAAGAGGA | 600 |
| ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA CCTCATACAC AGTTTAAAGT TGCTGTTTAC | 660 |
| GTTCTGCAAA AAGAAGAAGG TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA | 720 |
| TTCTTCTTCC GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG | 780 |
| GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAATTGA TTAGCCCTGT GGCTTTAGAA | 840 |
| GAAGGTATGA GATTGCGAT TCGTGAAGGT GGTCTGACAA TCGGTGCTGG A | 891 |

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

| | |
|--|-----|
| AACATGATCA CCGGTGCTGC GCAGATGGAC GGCGCGATCC TGGTAGTTGC TGCGACTGAC | 60 |
| GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC | 120 |
| ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT | 180 |
| GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC | 240 |
| GTTCTGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG | 300 |
| GAAGTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT TGACAAGCCG | 360 |
| TTCTTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT | 420 |
| CGTGTAGAAC GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG | 480 |
| ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT | 540 |
| GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT | 600 |
| CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC TGAAGTGTAC | 660 |
| ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG | 720 |
| TTCTACTTCC GTACTACTGA CGTGAAGTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG | 780 |
| GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC | 840 |
| GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C | 891 |

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fibrobacter succinogenes*

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AACATGGTGA | CTGGTGCTGC | TCAGATGGAC | GGCGCTATCC | TCGTTGTTGC | CGCTACTGAC | 60 |
| GGTCCGATGC | CGCAGACTCG | CGAACACATC | CTTCTCGCTC | ACCAGGTTGG | CGTGCCGAAG | 120 |
| ATCGTCGTGT | TCATGAACAA | GTGCGACATG | GTTGACGATG | CTGAAATTCT | CGACCTCGTC | 180 |
| GAAATGGAAG | TTCGCGAACT | CCTCTCCAAG | TATGACTTCG | ACGGTGACAA | CACCCCGATC | 240 |
| ATCCGTGGTT | CCGCTCTCAA | GGCCCTCGAA | GGCGATCCGG | AATACCAGGA | CAAGGTCATG | 300 |
| GAACTCATGA | ACGCTTGCGA | CGAATACATC | CCGCTCCCGC | AGCGCGATAC | CGACAAGCCG | 360 |
| TTCCTCATGC | CGATCGAAGA | CGTGTTACAG | ATTACTGGCC | GCGGCACTGT | CGCTACTGGC | 420 |
| CGTATCGAAC | GCGGTGTCGT | TCGCTTGAAC | GACAAGGTTG | AACGTATCGG | TCTCGGTGAA | 480 |
| ACCACCGAAT | ACGTCATCAC | CGGTGTTGAA | ATGTTCCGTA | AGCTCCTCGA | CGACGCTCAG | 540 |
| GCAGGTGACA | ACGTTGGTCT | CCTCCTCCGT | GGTGCTGAAA | AGAAGGACAT | CGTCCGTGGC | 600 |
| ATGGTTCTCG | CAGCTCCGAA | GTCTGTCACT | CCGCACACCG | AATTTAAGGC | TGAAATCTAC | 660 |
| GTTCTCACGA | AGGACGAAGG | TGGCCGTCAC | ACGCCGTTCA | TGAATGGCTA | CCGTCCGCAG | 720 |
| TTCTACTTCC | GCACCACCGA | CGTTACTGGT | ACGATCCAGC | TCCCGBAAGG | TGTCGAAATG | 780 |
| GTTACTCCGG | GTGACACGGT | CACGATCCAC | GTGAACCTCA | TCGCTCCGAT | CGCTATGGAA | 840 |
| AAGCAGCTCC | GCTTCGCTAT | CCGTGAAGGT | GGACGTACTG | TTGGTGCTGG | C | 891 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Flavobacterium ferrugineum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

| | |
|--|-----|
| AACATGATCA CCGGTGCTGC CCAGATGGAC GGTGCTATCT TAGTTGTGGC TGCATCAGAC | 60 |
| GGTCCTATGC CTCAAACAAA AGAACACATC CTGCTTGCTG CCCAGGTAGG TGTACCTAAA | 120 |
| ATGGTTGTGT TTCTGAATAA AGTTGACCTC GTTGACGACG AAGAGCTCCT GGAGCTGGTT | 180 |
| GAGATCGAGG TTCGCGAAGA ACTGACTAAA CGCGGTTTCG ACGGCGACAA CACTCCAATC | 240 |
| ATCAAAGGTT CCGCTACAGG CGCCCTCGCT GGTGAAGAAA AGTGGGTAA AGAAATTGAA | 300 |
| AACCTGATGG ACGCTGTTGA CAGCTACATC CCACTGCCTC CTCGTCCGGT TGATCTGCCG | 360 |
| TTCCTGATGA GCGTAGAGGA CGTATTCTCT ATCACTGGTC GTGGTACTGT TGCTACCGGT | 420 |
| CGTATCGAGC GTGGCCGTAT CAAAGTTGGT GAGCCTGTTG AGATCGTAGG TCTGCAGGAG | 480 |
| TCTCCCCTGA ACTCTACCGT TACAGGTGTT GAGATGTTCC GCAAACCTCCT CGACGAAGGT | 540 |
| GAAGCTGGTG ATAACGCCGG TCTCCTCCTC CGTGGTGTG AAAAAACACA GATCCGTCGC | 600 |
| GGTATGGTAA TCGTTAAACC CGGTTCCATC ACTCCGCACA CGGACTTCAA AGGCGAAGTT | 660 |
| TACGTACTGA GCAAAGACGA AGGTGGCCGT CACACTCCAT TCTTCAACAA ATACCGTCCT | 720 |
| CAATTCTACT TCCGTACAAC TGACGTTACA GGTGAAGTAG AACTGAACGC AGGAACAGAA | 780 |
| ATGGTTATGC CTGGTGATAA CACCAACCTG ACCGTTAAAC TGATCCAACC GATCGCTATG | 840 |
| GAAAAAGGTC TGAAATTCGC GATCCGCGAA GGTGGCCGTA CCGTAGGTGC AGGA | 894 |

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

| | |
|---|-----|
| AATATGATTA CTGGTGCGGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC AGCAACAGAT | 60 |
| GGTCCTATGC CACAAACTCG TGAACACATC TTATTAGGTC GCCAAGTAGG TGTTCCATAC | 120 |
| ATCATCGTAT TCTTAAACAA ATGCGACATG GTAGATGACG AAGAGTTATT AGAATTAGTC | 180 |
| GAAATGGAAG TTCGTGAACT TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC | 240 |

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| | |
|---|-----|
| GTACGTGGTT CAGCATTACA AGCGTTAAAC GGCGTAGCAG AATGGGAAGA AAAAATCCTT | 300 |
| GAGTTAGCAA ACCACTTAGA TACTTACATC CCAGAACCAG AACGTGCGAT TGACCAACCG | 360 |
| TTCTTCTTTC CAATCGAAGA TGTGTTCTCA ATCTCAGGTC GTGGTACTGT AGTAACAGGT | 420 |
| CGTGTAGAAC GAGGTATTAT CCGTACAGGT GATGAAGTAG AAATCGTCGG TATCAAAGAT | 480 |
| ACAGCGAAAA CTACTGTAAC GGGTGTGAA ATGTTCCGTA AATTACTTGA CGAAGGTCGT | 540 |
| GCAGGTGAAA ACATCGGTGC ATTATTACGT GGTACCAAAC GTGAAGAAAT CGAACGTGGT | 600 |
| CAAGTATTAG CGAAACCAGG TTCAATCACA CCACACACTG ACTTCGAATC AGAAGTGTAC | 660 |
| GTATTATCAA AAGATGAAGG TGGTCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAA | 720 |
| TTCTATTTCC GTACAACAGA CGTGA CTGGT ACAATCGAAT TACCAGAAGG CGTGGAATG | 780 |
| GTAATGCCAG GCGATAACAT CAAGATGACA GTAAGCTTAA TCCACCCAAT TGCGATGGAT | 840 |
| CAAGGTTTAC GTTTCGCAAT CCGTGAAGGT GGCCGTACAG TAGGTGCAGG C | 891 |

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

| | |
|--|-----|
| AACATGATCA CCGGTGCGGC GCAAATGGAC GGAGCGATTT TGGTTGTTTC TGCAGCTGAT | 60 |
| GGCCCTATGC CTCAAAC TAG GGAGCATATC TTATTGTCTC GTCAAGTAGG CGTGCCTCAC | 120 |
| ATCGTTGTTT TCTTAAACAA ACAAGACATG GTAGATGACC AAGAATTGTT AGAACTTGTA | 180 |
| GAAATGGAAG TGC GCGAATT GTTGAGCGCG TATGAATTTT CTGGCGATGA CACTCCTATC | 240 |
| GTAGCGGGTT CAGCTTTAAG AGCTTTAGAA GAAGCAAAGG CTGGTAATGT GGGTGAATGG | 300 |
| GGTGAAAAAG TGCTTAAACT TATGGCTGAA GTGGATGCCT ATATCCCTAC TCCAGAAAGA | 360 |
| GAACTGAAA AAAC TTTCTT GATGCCGGTT GAAGATGTGT TCTCTATTGC GGGTAGAGGG | 420 |
| ACTGTGGTTA CAGGTAGGAT TGAAAGAGGC GTGGTGAAAG TAGGCGATGA AGTGGAATC | 480 |
| GTTGGTATCA GACCTACACA AAAACGACT GTAACCGGTG TAGAAATGTT TAGGAAAGAG | 540 |
| TTGGAAAAAG GTGAAGCCGG CGATAATGTG GCGGTGCTTT TGAGAGGAAC TAAAAAAGAA | 600 |

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| | |
|---|-----|
| GAAGTGAAC GCGGTATGGT TCTATGCAAA CCAGGTTCTA TCACTCCGCA CAAGAAATTT | 660 |
| GAGGGAGAAA TTTATGTCCT TTCTAAAGAA GAAGGCGGGA GACACACTCC ATTCTTCACC | 720 |
| AATTACCGCC CGCAATTCTA TGTGCGCACA ACTGATGTGA CTGGCTCTAT CACCCTTCCT | 780 |
| GAAGGCGTAG AAATGGTTAT GCCTGGCGAT AATGTGAAAA TCACTGTAGA GTTGATTAGC | 840 |
| CCTGTTGCGT TAGAGTTGGG AACTAAATTT GCGATTCGTG AAGGCGGTAG GACCGTTGGT | 900 |
| GCTGGT | 906 |

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

| | |
|--|-----|
| AACATGATCA CCGGCGCCGC TCAGATGGAC GGCGCGATCC TCGTGGTCGC CGCTACCGAC | 60 |
| GGCCCGATGG CCCAGACCCG TGAGCACGTG CTCCTGGCCC GCCAGGTCGG CGTGCCGGCC | 120 |
| CTGCTCGTGG CCCTGAACAA GTCGGACATG GTGGAGGACG AGGAGCTCCT CGAGCGTGTC | 180 |
| GAGATGGAGG TCCGGCAGCT GCTGTCCTCC AGGAGCTTCG ACGTCGACGA GGCCCCGGTC | 240 |
| ATCCGCACCT CCGCTCTGAA GGCCCTCGAG GGCGACCCCC AGTGGGTCAA GTCCGTCGAG | 300 |
| GACCTCATGG ATGCCGTGGA CGAGTACATC CCGGACCCGG TGC GCGACAA GGACAAGCCG | 360 |
| TTCTTGATGC CGATCGAGGA CGTCTTCACG ATCACC GGCC GTGGCACC GTTGACCGGT | 420 |
| CGCGCCGAGC GCGGCACCCT GAAGATCAAC TCCGAGGTCG AGATCGTCGG CATCCGCGAC | 480 |
| GTGCAGAAGA CCACTGTCAC CGGCATCGAG ATGTTCCACA AGCAGCTCGA CGAGGCCTGG | 540 |
| GCCGGCGAGA ACTGCGGTCT GCTCGTGCGC GGTCTGAAGC GCGACGACGT CGAGCGCGGC | 600 |
| CAGGTGCTGG TGGAGCCGGG CTCCATCACC CCGCACACCA ACTTCGAGGC GAACGTCTAC | 660 |
| ATCCTGTCCA AGGACGAGGG TGGGCGTCAC ACCCCGTTCT ACTCGAACTA CCGCGCGCAG | 720 |
| TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCACGC TGCCCGAGGG CACCGAGATG | 780 |
| GTCATGCCCC GCGACACCAC CGAGATGTCG GTCGAGCTCA TCCAGCCGAT CGCCATGGAG | 840 |
| GAGGGCCTCG GCTTCGCCAT CCGCGAGGGT GGCCGCACCG TGGGCTCCGG C | 891 |

T00271 E4958550

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

| | |
|---|-----|
| AACATGATCA CCGGCGCCGC GCAGATGGAC GGTGCGATCC TGGTGGTCGC CGCCACCGAC | 60 |
| GGCCCGATGC CCCAGACCCG CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC | 120 |
| ATCCTGGTAG CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC | 180 |
| GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCG ACGAGGACGC CCCGGTTGTG | 240 |
| CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT GGGTTGCCTC TGTCGAGGAA | 300 |
| CTGATGAACG CGGTCGACGA GTCGATTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC | 360 |
| CTGATGCCGG TCGAGGACGT CTTACCATT ACCGGCCGCG GAACCGTGGT CACCGGACGT | 420 |
| GTGGAGCGCG GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG | 480 |
| ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA CCAGGGCCAG | 540 |
| GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GCGTCAAGC GCGAGGACGT CGAGCGTGGC | 600 |
| CAGGTTGTCA CCAAGCCCGG CACCACCACG CCGCACACCG AGTTCGAAGG CCAGGTCTAC | 660 |
| ATCCTGTCCA AGGACGAGGG CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG | 720 |
| TTCTACTTCC GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG | 780 |
| GTGATGCCCC GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT CGCCATGGAC | 840 |
| GAAGGTCTGC GTTTCGCGAT CCGCGAGGGT GGCCGCACCG TGGGCGCCGG C | 891 |

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

"E496850" 10021

(A) ORGANISM: *Mycoplasma genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

| | |
|---|-----|
| AATATGATCA CAGGTGCTGC ACAAATGGAT GGAGCTATTC TAGTTGTTTC AGCAACTGAT | 60 |
| AGTGTGATGC CCCAAACCCG CGAGCACATC TTACTTGCCC GCCAAGTAGG GGTTCCTAAA | 120 |
| ATGGTAGTTT TTCTAAACAA GTGTGATATT GCTAGTGATG AAGAGGTACA AGAACTTGTT | 180 |
| GCTGAAGAAG TACGTGATCT GTTAACTTCC TATGGTTTTG ATGGTAAGAA CACTCCTATT | 240 |
| ATTTATGGCT CAGCTTTAAA AGCATTGGAA GGTGATCCAA AGTGGGAGGC TAAGATCCAT | 300 |
| GATTTGATTA AAGCAGTTGA TGAATGGATT CCAACTCCTA CACGTGAAGT AGATAAACCT | 360 |
| TTCTTATTAG CAATTGAAGA TACGATGACC ATTACTGGTA GAGGTACAGT TGTTACAGGA | 420 |
| AGAGTTGAAA GAGGTGAACT CAAAGTAGGT CAAGAAGTTG AAATTGTTGG TTTAAAACCA | 480 |
| ATTAGAAAAG CAGTTGTTAC TGGAATTGAA ATGTTCAAAA AGGAACTTGA TTCAGCAATG | 540 |
| GCTGGTGACA ATGCTGGGGT ATTATTACGT GGTGTTGAAC GTAAAGAAGT TGAAAGAGGT | 600 |
| CAAGTTTLAG CAAAACCAGG CTCTATTAAA CCGCACAGA AATTTAAAGC TGAGATCTAT | 660 |
| GCTTTAAAGA AAGAAGAAGG TGGTAGACAC ACTGGTTTTT TAAACGGTTA CCGTCCTCAA | 720 |
| TTCTATTTCC GTACCACTGA TGTAAGTGGT TCTATTGCTT TAGCTGAAAA TACTGAAATG | 780 |
| GTTCTACCTG GTGATAATGC TTCTATTACT GTTGAGTTAA TTGCTCCTAT CGCTTGTGAA | 840 |
| AAAGGTAGTA AGTTCTCAAT TCGTGAAGGT GGTAGAACTG TAGGGGCAGG C | 891 |

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

| | |
|--|-----|
| AACATGATTA CCGGCGCCGC ACAAATGGAC GGTGCAATCC TGGTATGTTT TGCTGCCGAC | 60 |
| GGCCCTATGC CGCAAACCCG CGAACACATC CTGCTGGCCC GTCAAGTAGG CGTACCTTAC | 120 |
| ATCATCGTGT TCATGAACAA ATGCGACATG GTCGACGATG CCGAGCTGTT CCAACTGGTT | 180 |
| GAAATGGAAA TCCGCGACCT GCTGTCCAGC TACGACTTCC CCGGCGACGA CTGCCCCGATC | 240 |

| | |
|---|-----|
| GTACAAGGTT CCGCACTGAA AGCCTTGGA GCGGATGCCG CTTACGAAGA AAAAATCTTC | 300 |
| GAAGTGGCTA CCGCATTGGA CAGATACATC CCGACTCCCG AGCGTGCCGT GGACAAACCA | 360 |
| TTCTTGCTGC CTATCGAAGA CGTGTCTCTC ATTTCCGGCC GCGGTACCGT AGTCACCGGC | 420 |
| CGTGTAGAGC GAGGTATCAT CCACGTTGGT GACGAGATTG AAATCGTCGG TCTGAAAGAA | 480 |
| ACCCAAAAAA CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGTCAG | 540 |
| GCGGGCGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC GTGAAGACGT AGAACGCGGT | 600 |
| CAGGTATTGG CCAAACGGGG TACTATCACT CCTCACACCA AGTTCAAAGC AGAAGTGTAC | 660 |
| GTATTGAGCA AAGAAGAGGG CGGCCCCCAT ACCCCGTTTT TCGCCAACTA CCGTCCCCAA | 720 |
| TTCTACTTCC GTACCACTGA CGTAACCGGC ACGATTACTT TGGAAAAAGG TGTGGAAATG | 780 |
| GTAATGCCGG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCTAT CGCTATGGAA | 840 |
| GAAGGTCTGC GCTTTGCGAT TCGCGAAGGC GGCCGTACCG TGGGTGCCGG C | 891 |

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rickettsia prowazekii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

| | |
|---|-----|
| AATATGATAA CTGGTGCCGC TCAGATGGAT GGTGCTATAT TAGTAGTTTC TGCTGCTGAT | 60 |
| GGTCCTATGC CTCAAACCTAG AGAACATATA TTACTGGCAA AACAGGTAGG TGTACCTGCT | 120 |
| ATGGTAGTAT TTTTGAATAA AGTAGATATG GTAGATGATC CTGACCTATT AGAATTAGTT | 180 |
| GAGATGGAAG TAAGAGAATT ATTATCAAAA TATGGTTTCC CTGGTAATGA AATACCTATT | 240 |
| ATTAAAGGTT CTGCACTTCA AGCTTTAGAA GGAAAACCTG AAGGTGAAAA AGCTATTAAT | 300 |
| GAGTTAATGA ATGCAGTAGA TACGTATATA CCTCAGCCTA TAGAGCTACA AGATAAACCT | 360 |
| TTTTTAATGC CAATAGAGGA TGTATTTTCT ATTTTCAGGCA GAGGTACCGT TGTAACCTGGT | 420 |
| AGAGTGGAGT CAGGCATAAT TAAGGTGGGT GAAGAAATTG AAATAGTAGG TCTAAAAAAT | 480 |
| ACGCAAAAAA CGACTTGTAC AGGTGTAGAA ATGTTTCAGAA AATTACTTGA TGAAGGACAA | 540 |
| TCTGGAGATA ATGTCGGTAT ATTACTACGT GGTACAAAAA GAGAAGAAGT AGAAAGAGGA | 600 |

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"E496660"

| | |
|--|-----|
| CAAGTACTTG CAAAACCTGG GAGCATAAAA CCGCATGATA AATTTGAAGC TGAAGTGTAT | 660 |
| GTGCTTAGTA AAGAGGAAGG TGGACGTCAT ACCCCATTTA CTAATGATTA TCGCCCACAG | 720 |
| TTCTATTTTA GAACAACAGA TGTTACCGGC ACAATAAAAT TGCCTTCTGA TAAGCAGATG | 780 |
| GTTATGCCTG GAGATAATGC TACTTTTTTCA GTAGAATTAA TTAAGCCGAT TGCTATGCAA | 840 |
| GAAGGGTTAA AATTCTCTAT ACGTGAAGGT GGTAGAACAG TAGGAGCCGG T | 891 |

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

| | |
|--|-----|
| AACATGATCA CCGGTGCTGC TCAGATGGAC GGCGCGATCC TGGTTGTTGC TGCGACTGAC | 60 |
| GGCCCGATGC CGCAGACCCG TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC | 120 |
| ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT | 180 |
| GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC | 240 |
| GTTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCATC | 300 |
| GAAGTGGCTG GCTTCCTGGA TTCTTATATT CCGGAACCAG AGCGTGCGAT TGACAAGCCG | 360 |
| TTCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTACCAGGT | 420 |
| CGTGATAGAGC GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG | 480 |
| ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT | 540 |
| GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT | 600 |
| CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC TGAAGTGTAC | 660 |
| ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG | 720 |
| TTCTACTTCC GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG | 780 |
| GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC | 840 |
| GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C | 891 |

(2) INFORMATION FOR SEQ ID NO: 165:

T0027" E4968660

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putida*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

| | |
|--|-----|
| ATGATCACTG GTGCTGCACA GATGGACGGC GCGATTCTGG TAGTCGCTTC AACAGACGGT | 60 |
| CCAATGCCAC AGACTCGTGA GCACATCCTG CTTTCTCGTC AGGTTGGCGT ACCATTTCATC | 120 |
| ATCGTATTCA TGAACAAATG TGACATGGTA GATGACGAAG AGCTGTTAGA GCTAGTTGAG | 180 |
| ATGGAAGTGC GTGAACTGTT ATCAGAATAC GATTTCCCAG GTGATGACTT ACCGGTAATC | 240 |
| CAAGGTTTCAG CTCTGAAAGC GCTAGAAGGC GAGCCAGAGT GGGAAGCAA AATCCTTGAA | 300 |
| TTAGCAGCGG CGCTGGATTC TTACATTCCA GAACCACAAC GTGACATCGA TAAGCCGTTC | 360 |
| CTACTGCCAA TCGAAGACGT ATTCTCAATT TCAGGCCGTG GTACAGTAGT AACAGGTCGT | 420 |
| GTTGAGCGTG GTATTGTACG CGTAGGCGAC GAAGTTGAAA TCGTTGGTGT ACGTGCGACA | 480 |
| ACTAAGACAA CGTGACTGCG TGTAGAAATG TTCCGTAAAC TGCTTGACGA AGGTCGTGCA | 540 |
| GGTGAGAACT GTGGTATTTT GTTACGTGGT ACTAAGCGTG ATGACGTAGA ACGTGGTCAA | 600 |
| GTATTAGCGA AGCCAGGTTC AATCAACCCA CACACTACTT TTGAATCAGA AGTTTACGTA | 660 |
| CTGTCAAAAAG AAGAAGGTGG TCGTCACACG CCATTCTTCA AAGGCTACCG TCCACAGTTC | 720 |
| TACTTCCGTA CAACTGACGT AACCAGGTACT ATCGAACTGC CAGAAGGCGT AGAGATGGTA | 780 |
| ATGCCAGGCG ATAACATCAA GATGGTAGTG AACTGATTT GCCCAATCGC GATGGACGAA | 840 |
| GGTTTACGCT TCGCAATCCG TGAAGGCGGT CGTACAGTGG T | 881 |

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*

0995943.1.12001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

| | |
|---|-----|
| AACATGATCA CGGGCGCGGC GCAGATGGAC GGAGCGATTG TGGTGGTGTC CGCGGCCGAC | 60 |
| GGCCCGATGC CCCAGACGCG TGAGCACATC CTGCTGGCCA GGCAGGTGGG CGTGCCCTAC | 120 |
| ATCGTCGTCT TCCTGAACAA GGTGGACATG CTGGACGATC CGGAGCTGCG CGAGCTGGTG | 180 |
| GAGATGGAGG TGCGCGACCT GCTCAAGAAG TACGAGTTCC CGGGCGACAG CATCCCCATC | 240 |
| ATCCCTGGCA GCGCGCTCAA GGCCTGGAG GGAGACACCA GCGACATCGG CGAGGGAGCG | 300 |
| ATCCTGAAGC TGATGGCGGC GGTGGACGAG TACATCCCGA CGCCGCAGCG TGCGACGGAC | 360 |
| AAGCCGTTCC TGATGCCGGT GGAAGACGTG TTCTCCATCG CAGGCCGAGG AACGGTGGCG | 420 |
| ACGGGCCGAG TGGAGCGCGG CAAGATCAAG GTGGGCGAGG AAGTGGAGAT CGTGGGGATC | 480 |
| CGTCCGACGC AGAAGACGGT CATCACGGGG GTGGAGATGT TCCGCAAGCT GCTGGACGAG | 540 |
| GGCATGGCGG GAGACAACAT CGGAGCGCTG CTGCGAGGCC TGAAGCGCGA GGACCTGGAG | 600 |
| CGTGGGCAGG TGCTGGCGAA CTGGGGGAGC ATCAACCCGC ACACGAAGTT CAAGGCGCAG | 660 |
| GTGTACGTGC TGTCGAAGGA AGAGGGAGGG CGGCACACGC CGTTCTTCAA GGGATACCGG | 720 |
| CCGCAGTTCT ACTTCCGGAC GACGGACGTG ACCGGAACGG TGAAGCTGCC GGACAACGTG | 780 |
| GAGATGGTGA TGCCGGGAGA CAACATCGCC ATCGAGGTGG AGCTCATTAC TCCGGTCGCC | 840 |
| ATGGAGAAGG AGCTGCCGTT CGCCATCCGT GAGGGTGGCC GCACGGTGGG CGCCGGC | 897 |

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

| | |
|---|-----|
| AACATGATCA CTGGTGCCGC TCAAATGGAC GGAGCTATCC TTGTAGTTGC TTCAACTGAT | 60 |
| GGACCAATGC CACAACTCG TGAGCACATC CTTCTTTCAC GTCAGGTGGG TGTTAAACAC | 120 |
| CTTATCGTGT TCATGAACAA AGTTGACCTT GTTGATGACG AAGAGTTGCT TGAATTAGTT | 180 |
| GAGATGGAAA TTCGTGACCT TCTTTCAGAA TACGATTTC CAGGTGATGA CCTTCCAGTT | 240 |
| ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GCGGACACTA AATTGGAAGA CATCATCATG | 300 |

| | |
|---|-----|
| GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC TGACAAACCA | 360 |
| TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC GTGGTACAGT TGCTTCAGGA | 420 |
| CGTATCGACC GTGGTACTGT TCGTGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA | 480 |
| GAAACTAAAA AAGCTGTTGT TACTGGTGTG GAAATGTTCC GTAAACAACT TGACGAAGGT | 540 |
| CTTGCAGGAG ACAACGTAGG TATCCTTCTT CGTGGTGTTC AACGTGACGA AATCGAACGT | 600 |
| GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTA | 660 |
| TATATCCTTT CTAAAGACGA AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA | 720 |
| CAATTCTACT TCCGTACAAC TGACGTAACA GGTTCATCG AACTTCCAGC AGGTACAGAA | 780 |
| ATGGTTATGC CTGGTGATAA CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA | 840 |
| GAACAAGGTA CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT | 894 |

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiobacillus cuprinus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

| | |
|---|-----|
| AACATGATCA CCGGTGCGGC CCAGATGGAC GGCGCCATCC TGGTCGTGTC CGCCGCCGAC | 60 |
| GGCCCCATGC CCCAAACCCG CGAGCACATC CTGCTGGCGC GTCAGGTGGG CGTGCCCTAC | 120 |
| ATCATCGTGT TCCTCAACAA GTGCGACATG GTCGACGACG CCGAGCTGCT CGAACTCGTC | 180 |
| GAGATGGAAG TGC GCGAGCT GCTGTCCAAG TACGACTTCC CCGGTGACGA CACCCCATC | 240 |
| ATCAAGGGCT CGGCCAAGCT GGCCCTCGAA GGCGACAAGG GCGAACTGGG CGAAGGCGCC | 300 |
| ATTCTCAAGC TGGCCGAGGC CCTGGACACC TACATCCCCA CGCCCGAGCG GGCCGTCGAC | 360 |
| GGCGCGTTCC TCATGCCCCT GGAAGACGTG TTCTCCATCT CCGGGCGCGG CACGGTGGTC | 420 |
| ACCGGGCGTG TGGAGCGCGG CATCATCAAG GTCGGCGAGG AAATCGAGAT TGTCGGCCTC | 480 |
| AAGCCCCACC TCAAGACCAC CTGCACCGGC GTGGAAATGT TCAGGAAGCT GCTCGACCAG | 540 |
| GGCCAGGCCG GCGACAACGT CGGCATCTTG CTGCGCGGCA CCAAGCGCGA GGAAGTCGAG | 600 |
| CGCGGCCAGG TGCTGTGCAA ACCCGGCTCG ATCAAGCCCC ACACCCACTT CACCGCCGAG | 660 |

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| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GTGTACGTGC | TGAGCAAGGA | CGAGGGCGGC | CGCCACACCC | CCTTCTTCAA | CAACTACCGC | 720 |
| CCGCAGTTCT | ACTTCCGCAC | CACCGACGTC | ACCGGCGCCA | TCGAACTGCC | CAAGGACAAG | 780 |
| GAAATGGTCA | TGCCCCGGCGA | TAATGTGAGC | ATCACCGTCA | AGCTCATCGC | CCCCATCGCC | 840 |
| ATGGAAGAAG | GCCTGCGCTT | CGCCATCCGC | GAAGGCGGCC | GCACCGTCGG | CGCCGGC | 897 |

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| AATATGATCA | CGGGTGCTGC | GCAGATGGAC | GGTGGTATTC | TCGTCGTGTC | TGCGCCTGAC | 60 |
| GGCGTTATGC | CACAGACGAA | GGAGCATCTT | CTGCTCGCCC | GTCAGGTTGG | TGTTCCCTCC | 120 |
| ATCATTGTTT | TTTTGAACAA | GGTTGATTTG | GTTGATGATC | CTGAGTTGCT | AGAGCTGGTG | 180 |
| GAAGAAGAGG | TGCGTGATGC | GCTTGCTGGA | TATGGGTTTT | CGCGTGAGAC | GCCTATCGTC | 240 |
| AAGGGGTCTG | CGTTTAAAGC | TCTGCAGGAT | GGCGCTTCCC | CGGAGGATGC | AGCTTGTATT | 300 |
| GAGGAACTGC | TTGCGGCCAT | GGATTCTTAC | TTTGAAGACC | CAGTGCGTGA | CGACGCAAGA | 360 |
| CCTTTCTTGC | TCTCTATCGA | GGATGTGTAC | ACTATTTCTG | GGCGTGGTAC | CGTTGTCACG | 420 |
| GGGCGCATCG | AATGTGGGGT | AATTAGTCTG | AATGAAGAGG | TCGAGATCGT | CGGGATTAAG | 480 |
| CCCACTAAGA | AAACAGTGGT | TACTGGCATT | GAGATGTTTA | ATAAGTTGCT | TGATCAGGGA | 540 |
| ATTGCAGGTG | ATAACGTGGG | GCTGCTTTTG | CGCGGGGTGG | ATAAAAAAGA | GGTTGAGCGC | 600 |
| GGTCAGGTGC | TTTCTAAGCC | CGGTTCTATT | AAGCCACACA | CCAAGTTTGA | GGCGCAGATC | 660 |
| TACGTGCTCT | CTAAGGAAGA | GGGTGGCCGT | CACAGTCCTT | TTTTTCAAGG | TTATCGTCCG | 720 |
| CAGTTTTTATT | TTAGAACTAC | TGACATTACC | GGTACGATTT | CTCTTCCTGA | AGGGGTAGAC | 780 |
| ATGGTGAAGC | CGGGGGATAA | CACCAAGATT | ATAGGTGAGC | TCATCCACCC | GATAGCTATG | 840 |
| GACAAGGGTC | TGAAGCTTGC | GATTCGTGAA | GGGGGGCGCA | CTATTGCTTC | TGGT | 894 |

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

T0021 "E495350

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ureaplasma urealyticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

| | |
|--|-----|
| AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC TGCATCTGAT | 60 |
| GGGGTTATGG CTCAAACATA AGAACATATT TTATTAGCAC GTCAAGTTGG TGTTCACAAA | 120 |
| ATCGTTGTTT TCTTAAACAA ATGTGATTTT ATGACAGATC CAGATATGCA AGATCTTGTT | 180 |
| GAAATGGAAG TTCGTGAATT ATTATCTAAA TATGGATTTG ATGGCGATAA CACACCAGTT | 240 |
| ATTCGTGGTT CAGGTCTTAA GGCTTTAGAA GGAGATCCAG TTTGAGAAGC AAAAATTGAT | 300 |
| GAATTAATGG ACGCAGTTGA TTCATGAATT CCATTACCAG AACGTAGTAC TGACAAACCA | 360 |
| TTCTTATTAG CAATTGAAGA TGTATTCACA ATTTACAGGAC GTGGTACAGT AGTAACTGGA | 420 |
| CGTGTGTAAC GTGGTGTATT AAAAGTTAAT GATGAGGTTG AAATTGTTGG TCTAAAAGAC | 480 |
| ACTCAAAAAA CTGTTGTTAC AGGAATTGAA ATGTTTAGAA AATCATTAGA TCAAGCTGAA | 540 |
| GCTGGTGATA ATGCTGGTAT TTTATTACGT GGTATTAAAA AAGAAGATGT TGAACGTGGT | 600 |
| CAAGTACTTG TAAAACCAGG ATCAATTAAA CCTCACCGTA CTTTTACTGC TAAAGTTTAT | 660 |
| ATTCTTAAAA AAGAAGAAGG TGGACGTCAT ACACCTATTG TTTCAGGATA CCGTCCACAA | 720 |
| TTCTATTTTA GAACAACAGA TGTAACAGGT GCTATTTTAT TACCTGCTGG TGTGATTTG | 780 |
| GTTATGCCAG GTGATGACGT TGAAATGACT GTAGAATTAA TTGCTCCAGT TGCGATTGAA | 840 |
| GATGGATCTA AATTCTCAAT CCGTGAAGGT GGTAAACTG TAGGTCATGG T | 891 |

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Wolinella succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

"T002T" E495550

[illegible]

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION:6
(D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION:12
(D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION:18
(D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TARTCNGTRA ANGCYTCNAC RCACAT

26

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TCTTTAGCAG AACAGGATGA A

21

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GAATAATTCC ATATCCTCCG

20

0909043 "E4968660
T002T"